GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 20.87 Seconds
(without alignments)
2122.529 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2468	100.0	461	1	A35356	tumor necrosis fac
2	1512	61.3	474	2	B38634	tumor necrosis fac
3	1477	59.8	459	2	I48854	gene murine tumour
4	381.5	15.5	349	2	D72175	G2R protein - vari
5	379.5	15.4	348	2	T28623	hypothetical prote
6	379.5	15.4	349	2	D36858	gene G4R protein -
7	360.5	14.6	326	1	GQVZML	T2 protein - myxom
8	341.5	13.8	435	2	I54182	tumor necrosis fac
9	328	13.3	325	2	B43692	T2 protein - rabbi
10	317.5	12.9	277	2	A60771	B-cell activation
11	290.5	11.8	651	2	JC7705	death receptor-6 -
12	258.5	10.5	305	2	A46476	B cell-associated
13	251.5	10.2	416	1	JN0006	nerve growth facto
14	241	9.8	595	2	A42086	CD30 antigen precu
15	229.5	9.3	271	2	S12783	OX40 antigen precu
16	223.5	9.1	272	2	I48700	gene ox40 protein
17	219.5	8.9	493	2	JC5486	membrane glycoprot
18	217	8.8	277	2	I37552	OX40 homolog - hum
19	210	8.5	427	1	GQHUN	nerve growth facto
20	198	8.0	461	2	JC4302	tumor necrosis fac
21	197	8.0	256	2	B32393	T-cell antigen 4-1
22	197	8.0	425	1	A26431	nerve growth facto
23	191.5	7.8	454	1	GQMST1	tumor necrosis fac
24	185.5	7.5	461	1	GQRTT1	tumor necrosis fac
25	185	7.5	255	2	I38426	lymphocyte activat
26	183.5	7.4	455	1	GQHUT1	tumor necrosis fac
27	166.5	6.7	1367	1	S48478	glucan 1,4-alpha-g
28	165	6.7	770	2	T51024	related to C2H2 zi
29	161.5	6.5	1203	2	T17415	mycelial surface a
30	161	6.5	1372	2	T25933	hypothetical prote
31	159.5	6.5	2232	2	T34434	hypothetical prote
32	158	6.4	1274	2	T42017	cysteine rich prot
33	156.5	6.3	383	2	T46707	proteophosphoglyca
34	154.5	6.3	1428	2	T08852	lustrin A - Califo
35	153.5	6.2	3507	2	T34513	hypothetical prote
36	150	6.1	801	2	T29018	hypothetical prote
37	148.5	6.0	1032	2	T34433	hypothetical prote
38	148	6.0	327	2	A46484	apoptosis-mediatin
39	147	6.0	438	2	T31889	hypothetical prote
40	147	6.0	600	2	S07638	spore coat protein
41	145	5.9	742	2	I37225	leucocyte antigen
42	144	5.8	314	2	I37383	FAS soluble protei
43	143.5	5.8	324	2	JC2395	Fas antigen precur
44	143	5.8	534	2	T39903	serine-rich protei
45	143	5.8	3942	2	T42730	Bassoon protein -

ALIGNMENTS

RESULT 1
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A;Reference number: A35356; MUID:90260639
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A;Reference number: A36475; MUID:91045991
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellul
A;Reference number: A48416; MUID:91370690
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A;Reference number: A36007; MUID:90349572
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor
A;Reference number: A23666; MUID:91056048
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>

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R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             100.0%;  Score 2468;  DB 1;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-134;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||||
Db    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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RESULT   2
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match             61.3%;  Score 1512;  DB 2;  Length 474;
  Best Local Similarity   63.0%;  Pred. No. 3e-79;
  Matches  293;  Conservative   50;  Mismatches  114;  Indels    8;  Gaps    6;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
          ||| |:| ||   |:|||  | :|||| ||| |||| |:: :|||: |||||:|| |
Db      1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy     60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
          ||: | || |||||||  || | |||:||    |||| | |::|||| :|||::|||:|
Db     61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120

Qy    120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
          |  | ||||    | || |  | || ||||||       :|:|| |||||||:||||||:
Db    121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180

Qy    179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
          ||||:||:::|||||||  ||||   ||| |  |  ::: ||  ||||     | ||  |
Db    181 CRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP- 239

Qy    239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
          | |  :| :|  | || |  :||:|||||||:||||::|:|||:|: | |||| ||||:
Db    240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQRKKKPSCLQRD 298

Qy    298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
          |||||:| :|::   | |||||| ||||||||||||||| |||||    |||  : ||
Db    299 AKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQ 358

Qy    357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
          |  |||||:  |||| | ||| |||||||||||||||||||:|:|| |: || ||
Db    359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 418

Qy    417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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Db    419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461


RESULT   3
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>


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  Best Local Similarity   63.8%;  Pred. No. 2.8e-77;
  Matches  287;  Conservative   47;  Mismatches  108;  Indels    8;  Gaps    6;

Qy      16 LWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSPGQHAKVFCTKTSDTV 74
           |||  | :||||  ||| ||||  |:: :||||: |||||:|| |||: | || ||||||
Db       1 LWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNKTSDTV 60

Qy      75 CDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEG- 133
           |  || | |||:||    |||| | ||:|||||:|||::|||:| |  | ||||    |
Db      61 CADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS 120

Qy     134 CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN 193
           || |  | || ||||||       :|:|| |||||||:||||||:||||:||:::|||||
Db     121 CRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICSILAIPGN 180

Qy     194 ASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 253
           || ||||   ||| |  |  ::: ||  ||||     | ||  |  | |  :| :|  |
Db     181 ASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP--SILTSLGSTPIIEQ 238

Qy     254 ST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQ 312
           || |  :||:|||||||:||||::|:||| |: | |||| ||||:|||||:| :|::
Db     239 STKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVPDEKSQDAV 298

Qy     313 GPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EASGAGEARASTGSSDSS 371
           | |||||| |||||||||||||| |||||    |||  : || |: |||||:  ||||
Db     299 GLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISDSS 358

Qy     372 PGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFR 431
           | ||| |||||||||||||||||||||||:|:|| |: || ||||||||||:|||  :
Db     359 HGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASPKDEQVPFSQEECPSQ 418

Qy     432 SQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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Db     419 SPYETTETL--QSHEKPLPLGVPDMGMKPS 446


RESULT   4
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology


  Query Match             15.5%;  Score 381.5;  DB 2;  Length 349;
  Best Local Similarity   38.1%;  Pred. No. 5.7e-15;
  Matches   80;  Conservative   23;  Mismatches   86;  Indels   21;  Gaps    7;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           || | |   |:  ||  :   :|| | || :|   |   ::| | |   |:|   | :
Db      24 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | ||||  ||:|:||||::|    |||| | ||:|| |    ||: |    ||  |:||:
Db      81 PACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT-----ST 203
             |   ||:| ||  ||:| | |||| | |        :| |    :|   |      |
Db     141 -GHTSVGDVICSPCGFGTYSYTVSSTDKCEP--------VPNNTFNYIDVEITLYPVNDT 191

Qy     204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
           | ||:   |     |   ::   ||   |
Db     192 SCTRTTTTGLSESILTSELTITMNHTDCNP 221


RESULT   5
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir
A;Reference number: Z20488; MUID:94088747
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology


  Query Match             15.4%;  Score 379.5;  DB 2;  Length 348;
  Best Local Similarity   37.6%;  Pred. No. 7.4e-15;
  Matches   79;  Conservative   24;  Mismatches   86;  Indels   21;  Gaps    7;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           || | |   |:  ||  :   :|| | || :|   |   ::| | |   |:|   | :
Db      23 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 79

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | ||||  ||:|:||||::|    |||| | ||:|| |    ||: |    ||  |:||:
Db      80 PACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGVS 139

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT-----ST 203
             |   ||:| ||  ||:|:| || | | |        :| |    :|   |      |
Db     140 -GHTSVGDVICSPCGFGTYSHTVSSADKCEP--------VPNNTFNYIDVEITLYPVNDT 190

Qy     204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
           | ||:   |     |   ::   ||   |
Db     191 SCTRTTTTGLSESILTSELTITMNHTDCNP 220


RESULT   6
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
```

```
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>


  Query Match             15.4%;  Score 379.5;  DB 2;  Length 349;
  Best Local Similarity   37.6%;  Pred. No. 7.4e-15;
  Matches   79;  Conservative   24;  Mismatches   86;  Indels   21;  Gaps    7;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           || | |    |:  ||  :   :||  | || :|    |   ::| |  |   |:|   | :
Db      24 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | ||||  ||:|:||||::|    |||| | ||:|| |    ||: |    ||  |:||:
Db      81 PACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT-----ST 203
             |   ||:| ||  ||:|:| || | | |        :| |    :|   |       |
Db     141 -GHTSVGDVICSPCGFGTYSHTVSSADKCEP--------VPNNTFNYIDVEITLYPVNDT 191

Qy     204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
           | ||:   |      |   ::    ||   |
Db     192 SCTRTTTTGLSESILTSELTITMNHTDCNP 221


RESULT   7
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             14.6%;  Score 360.5;  DB 1;  Length 326;
  Best Local Similarity   36.9%;  Pred. No. 8.4e-14;
  Matches   75;  Conservative   29;  Mismatches   86;  Indels   13;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           ||  : |  ||  :|  :   :||: | || :|   |   ||||  |:: |:|   |
Db      20 PYGADRGK-CRGNDY--EKDGLCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHA 76

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | |:||  ||:    |:|:| : ::|:| |  | || |  |||||:|||  ||  |:||:
Db      77 PACVSCRGRCTGHLSESQSCDKTRDRVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYGVS 136

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN--ASMDAVCTSTSPTRS 208
             | ||:|  |   |:|:  |||: |      | :::  |     |  ||:|:
Db     137 -GHTRTGDVLCTKCPRYTYSDAVSSTETCT--SSFNYISVEFNLYPVNDTSCTTTA---- 189

Qy     209 MAPGAVHLPQPVSTRSQHTQPTP 231
             |   |      |    ||   |
Db     190 -GPNEVVKTSEFSVTLNHTDCDP 211


RESULT   8
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
A;Reference number: I54182; MUID:93252381
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology


  Query Match             13.8%;  Score 341.5;  DB 2;  Length 435;
  Best Local Similarity   29.1%;  Pred. No. 1.3e-12;
  Matches  120;  Conservative   45;  Mismatches  141;  Indels  107;  Gaps   25;

Qy       2 APVAVWAALAVGL-ELWAAA--HALPAQVAFTPYAPEPGSTCR--LREYYDQTAQMCCSK 56
           ||   |  | :|| | ||:   |:|      ||| |   |||   :|||:   ::|||:
Db       9 APGLAWGPLVLGLFGLLAASQPQAVP------PYASE-NQTCRDQEKEYYEPQHRICCSR 61

Qy      57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQV----ETQACTR 112
           | || :    |::  |||| :| :::| : ||::  |  |       | |     |   ||
Db      62 CPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCR---PCDPVMGLEEIAPCTS 118

Qy     113 EQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV------CKPCAP 166
           ::   | |:|| :||    | |  |  |  | ||         |  | |      | ||
Db     119 KRKTQCRCQPGMFCAAWALE-CTHCELLSDCPPG-----TEAELKDEVGKGNNHCVPCKA 172

Qy     167 GTFSNTTSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPG--------AV 214
           | | ||:| :  |:||  |      | | || |  |  |   :|   : |          ||
Db     173 GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPPEMSGTMLMLAV 230

Qy     215 HLPQP----VST------RSQHTQPTPEPSTAPSTSFLL---PMGPSP-PAEGS------ 254
            ||      ::|      :|        ||       ||   | |  | |  ||
```

```
Db    231 LLPLAFFLLLATVFSCIWKS-------HPSLCRKLGSLLKRRPQGEGPNPVAGSWEPPKA 283

Qy    255 --------------TGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
                       :|| : ||    |: |  :|  ||         :: || | ||
Db    284 HPYFPDLVQPLLPISGDVS-PVS--TGLPAAPVLEAGVPQ-------QQSPLDLTRE--- 330

Qy    301 PHL-PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPG 352
          | | | ::::   |    |:       :  |:  : :      |    |  ||
Db    331 PQLEPGEQSQVAHGTNGIHV-------TGGSMTITGNIYIYNGPVLGGPPGPG 376


RESULT   9
B43692
T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A;Reference number: A43692; MUID:87321103
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>


  Query Match             13.3%;  Score 328;  DB 2;  Length 325;
  Best Local Similarity   36.9%;  Pred. No. 6e-12;
  Matches   66;  Conservative   28;  Mismatches   71;  Indels   14;  Gaps    6;

Qy     31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
          ||:   |  |   :|  :   :||: | || :|   |   |:|||  ||| |:|   |
Db     20 PYSSNQGK-CGGHDY--EKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHA 76

Qy     91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
          | |:||   |:    |:| | |  :|:| |  | || |  | |||:|||  ||  |:||:
Db     77 PACVSCRGPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQNGCRICAPQTKCPAGYGVS 136

Qy    151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI-----PGNASMDAVCTSTS 204
              |   | :|: | | |:|:: | |: |      | :::     | |   :  ||:|:
Db    137 -GHTRAGDTLCEKCPPHTYSDSLSPTERCGTS--FNYISVGFNLYPVN---ETSCTTTA 189


RESULT  10
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             12.9%;  Score 317.5;  DB 2;  Length 277;
  Best Local Similarity   26.7%;  Pred. No. 2e-11;
  Matches   92;  Conservative   32;  Mismatches  124;  Indels   97;  Gaps   11;

Qy     23 LPAQVA-----FTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS 77
          || |         |   ||| : || ::|   :    ||| | |||     ||: ::| |
Db      4 LPLQCVLWGCLLTAVHPEPPTACREKQYLINS--QCCSLCQPGQKLVSDCTEFTETECLP 61

Qy     78 CEDSTYTQLWNWVPEC-------LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
          | :| :   ||    |         : | |         |  | | : |||  ||:|
Db     62 CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ------QKGTSETDTICTCEEGWHCT--- 112

Qy    131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN---- 186
           | |  |   | | ||||| :  |  || :|:||  | ||| :|: : | |   |
Db    113 SEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDL 172

Qy    187 VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMG 246
          ||   |    | ||      |::
Db    173 VVQQAGTNKTDVVCGPQDRLRAL---------------------------------- 195

Qy    247 PSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPH---- 302
                      : : :| |:    ||::     | : :| |||       | ||
Db    196 ------------VVIPIIFGILFAILLVL-----VFIKKVAKKP-----TNKAPHPKQE 232

Qy    303 -----LPAD-KARGTQGPEQQHLLITAPSSSSSSLESSASALDRR 341
               | |     |  | |: |    | :     ||  |  :|:
Db    233 PQEINFPDDLPGSNTAAPVQETLHGCQPVTQEDGKESRISVQERQ 277


RESULT  11
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belo
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted


  Query Match             11.8%;  Score 290.5;  DB 2;  Length 651;
  Best Local Similarity   31.7%;  Pred. No. 1.6e-09;
  Matches   70;  Conservative   24;  Mismatches   96;  Indels   31;  Gaps    6;

Qy     51 QMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQAC 110
          :: | ||  | :    |||::   |  | | |:|:  | :  |  |   |    :|   |
```

```
Db     49 ELICDKCPAGTYVSKHCTKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPMIEKTHC 108

Qy    111 TREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFS 170
          |   :| |||  | :      :    | |   |  |:|| : |||| || |||| ||||
Db    109 TALTDRECTCLSGTF------QINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFS 162

Qy    171 NTTSSTDICRPHQIC---NVVAI-PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQH 226
          :  ||   |: :  |   |:| : ||    | || | :          ||   |  |
Db    163 DVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVCXSPA----------SLPN-TSLTSSD 211

Qy    227 TQPTPEPSTAPSTSFL----------LPMGPSPPAEGSTGD 257
           |   |   || |::|          |   |:|     | :
Db    212 AQADGETYEAPPTAYLPKGLNSSVFDLSSSPAPRVSNGTAE 252


RESULT  12
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>


  Query Match             10.5%;  Score 258.5;  DB 2;  Length 305;
  Best Local Similarity   22.8%;  Pred. No. 5.1e-08;
  Matches   87;  Conservative   37;  Mismatches  142;  Indels  115;  Gaps   14;

Qy      5 AVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAK 64
          |:|  |   : |                        ||  ::|       ||  | ||
Db      9 ALWGCLLTAVHLGQCV-----------------TCSDKQYLHD--GQCCDLCQPGSRLT 48

Qy     65 VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQ---VETQACTREQNRICTCR 121
           ||    | |  |:   ::  ||    |      |  :|   |: :  | | : :|||:
Db     49 SHCTALEKTQCHPCDSGEFSAQWNREIRCHQ-HRHCEPNQGLRVKKEG-TAESDTVCTCK 106

Qy    122 PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRP 181
           | :|     : |  ||    | |||||    |||:| || ||  | ||| :|  : | |
Db    107 EGQHCT---SKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYP 163

Qy    182 HQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 237
            |       |   | :  : :|   |  |::
Db    164 WTSCEDKNLEVLQKGTSQTNVICGLKSRMRAL---------------------------- 195

Qy    238 STSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
                        :|| : : :|  |: :        : :| |||   :
Db    196 ------------------LVIPVVMGILITIFGVFL-------YIKKVVKKP---KDN 225


Qy    298 AKVPHLPADK-----------ARGTQGPEQQHLLITAPSSSSSSLESSASALDR------ 340
            :|  || :               |  | |: |    | :     ||  |  :|
Db    226 EMLP--PAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQVTDSI 283

Qy    341 --RAPTRNQPQAPGVEASGAG 359
          | |  |    ||    | |
Db    284 ALRPPGLN----PGTAFGGDG 300


RESULT  13
JN0006
nerve growth factor receptor, low affinity precursor - chicken
N;Alternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R
Neuron 2, 1123-1134, 1989
A;Title: Structure and developmental expression of the nerve growth factor receptor i
A;Reference number: JN0006; MUID:90166579
A;Accession: JN0006
A;Molecule type: mRNA
A;Residues: 1-416 <LAR>
A;Experimental source: embryonic chick brain
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140
A;Accession: A60504
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C;Comment: The cysteine-rich region of the extracellular domain may form part or all
C;Comment: This protein is thought to form a high-affinity receptor when it associate
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;24-57/Domain: NGF receptor repeat homology <NG1>
F;59-100/Domain: NGF receptor repeat homology <NG2>
F;101-139/Domain: NGF receptor repeat homology <NG3>
F;141-181/Domain: NGF receptor repeat homology <NG4>
F;189-237/Region: serine/threonine-rich
F;240-261/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             10.2%;  Score 251.5;  DB 1;  Length 416;
  Best Local Similarity   25.1%;  Pred. No. 1.7e-07;
  Matches   89;  Conservative   48;  Mismatches  164;  Indels   53;  Gaps   16;

Qy     23 LPAQVAFTPYAPEPGS--TCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED 80
          :|  :   |  |  ||   |  : |   |:  ||  |: |:     |   : |||: | |
Db      5 VPLLLLLLPAGPTWGSKEKCLTKMY--TTSGECCKACNLGEGVVQPC-GVNQTVCEPCLD 61

Qy     81 S-TYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAP 139
          | ||:   :    |  | ::|      :  |    : :| |  |::    : |    |
Db     62 SVTYSDTVSATEPCKPC-TQCVGLHSMSAPCVESDDAVCRCAYGYF----QDELSGSCKE 116

Qy    140 LRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAV 199
          |  |||:  |  :: | ||: |  ||||:  :  | | |  ||       |  |
Db    117 CSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANFVDPCLPCTICE-----ENEVMVKE 171

Qy    200 CTSTSPT--RSMAP-GAVHLPQPVSTRSQHTQPTPEP----------STAPSTSFLLPM 245
          ||:||    | : |    | |    : |      |||           :|  :      |
Db    172 CTATSDAECRDLHPRWTTHTPSLAGSDS------PEPITRDPFNTEGMATTLADIVTTVM 225

Qy    246 GPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304
          | | |     | |  :||   :    |  :::|:|  :     |:   | | :    : |
```

```
Db    226 GSSQPVVSRGTADNLIPVYCSI----LAAVVVGLVAYIAF---KRWNSCKQNKQGANNRP 278

Qy    305 ADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGA 358
Db    279 VNQ---TPSPEGEKL------HSDSGISVDSQSLHDQQPPNQSTQGPAPKGDGS 323


RESULT  14
A42086
CD30 antigen precursor - human
N;Alternate names: Ki-1 antigen; nerve growth factor receptor family member CD30
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C;Accession: A42086
R;Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein, H.
Cell 68, 421-427, 1992
A;Title: Molecular cloning and expression of a new member of the nerve growth factor rec
A;Reference number: A42086; MUID:92154659
A;Accession: A42086
A;Molecule type: mRNA
A;Residues: 1-595 <DUR>
A;Cross-references: GB:M83554; NID:g180095; PIDN:AAA51947.1; PID:g180096
A;Experimental source: HUT-102 cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:82088, NCBIP:82090)
C;Genetics:
A;Gene: GDB:CD30; D1S166E
A;Cross-references: GDB:131547; OMIM:153243
A;Map position: 1p36-1p36
C;Superfamily: NGF receptor repeat homology
C;Keywords: glycoprotein; growth factor receptor; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-383/Domain: extracellular #status predicted <EXT>
F;384-407/Domain: transmembrane #status predicted <TMM>
F;408-595/Domain: intracellular #status predicted <CYT>
F;101,276/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             9.8%;  Score 241;  DB 2;  Length 595;
  Best Local Similarity   22.0%;  Pred. No. 9.7e-07;
  Matches  113;  Conservative   41;  Mismatches  183;  Indels  176;  Gaps   17;

Qy     11 AVGLELWAAAHALPAQVAFTPYAPEPGSTC--RLREYYDQTAQMCCSKCSPGQHAKVFCT 68
Db      7 ALGLLFLGALRAFPQDRPFE-------DTCHGNPSHYYDKAVRRCCYRCPMGLFPTQQCP 59

Qy     69 KTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCAL 128
Db     60 QRPTDCRKQCEPDYYL---DEADRCTACVTCSRDDLVEKTPCAWNSSRVCECRPGMFCST 116

Qy    129 SKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPG---------------------- 167
Db    117 SAVNSCARCFFHSVCPAGMIVKFPGTAQKNTVCEPASPGVSPACASPENCKEPSSGTIPQ 176

Qy    168 ---------TFSNTT---------------------------------------------- 173
Db    177 AKPTPVSPATSSASTMPVRGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQPCPEG 236

Qy    174 ----------------------------------------SSTDICRPHQICNVVAIPG 192
Db    237 SGDCRKQCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAWNSSRTCECRPGMICATSATNS 296

Qy    193 NASMDAVCTSTSPTRSMAPGAVHLPQ------------PVSTRSQHTQPTPE-----PST 235
Db    297 -------CARCVPYPICAAETVTKPQDMAEKDTTFEAPPLGTQPD-CNPTPENGEAPAST 348

Qy    236 APSTSFL--------LPMGPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQ 286
Db    349 SPTQSLLVDSQASKTLPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVVGSSAFLLCH 408

Qy    287 VKKKPLCLQREAKVPHL--PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPT 344
Db    409 ---RRACRKRIRQKLHLCYPVQ----TSQPKLE-LVDSRPRRSSTQLRSGASVTEPVAEE 460

Qy    345 R---NQPQAPGVEASGAGEARASTGSSDSSPGG 374
Db    461 RGLMSQPLMETCHSVGAAYLE-SLPLQDASPAG 492


RESULT  15
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A;Reference number: S12783; MUID:90214614
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>


  Query Match             9.3%;  Score 229.5;  DB 2;  Length 271;
  Best Local Similarity   27.1%;  Pred. No. 2e-06;
  Matches   79;  Conservative   28;  Mismatches   88;  Indels   97;  Gaps   14;

Qy      6 VW-----AALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYD--QTAQMCCSKCS 58
Db      3 VWVQQPTAFLLLGLSL------------------GVTVKLNCVKDTYPSGHKCCRECQ 42

Qy     59 PGQHAKVFCTKTSDTVCDSCEDSTYTQLWNW--VPECLSCGSRCSSDQVETQACTREQNR 116
Db     43 PGHGMVSRCDHTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSEL--KQNCTPTEDT 100

Qy    117 ICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETS---DVVCKPCAPGTFSNTT 173
Db    101 VCQCRPG------------------------TQPRQDSSHKLGVDCVPCPPGHFS--P 132

Qy    174 SSTDICRPHQICNV----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT-- 227
Db    133 GSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRS-----------LLATLLWETQRTTF 181

Qy    228 QPTPEPSTA--------PSTSFLL-PMGPSPPAEGSTGDFALPVGLIVGVTA 270
Db    182 RPTTVPSTTVWPRTSQLPSTPTLVAPEGPA---------FAVILGLGLGLLA 224


Search completed: August 21, 2002, 09:53:43
Job time: 31 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 09:54:07 ; Search time 13.41 Seconds
(without alignments)
1331.075 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2462	99.8	461	1	TR1B_HUMAN	P20333 homo sapien
2	1512	61.3	474	1	TR1B_MOUSE	P25119 mus musculu
3	379.5	15.4	349	1	VC22_VARV	P34015 variola vir
4	360.5	14.6	326	1	VT2_MYXVL	P29825 myxoma viru
5	341.5	13.8	435	1	TNR3_HUMAN	P36941 homo sapien
6	328	13.3	325	1	VT2_SFVKA	P25943 shope fibro
7	317.5	12.9	277	1	TNR5_HUMAN	P25942 homo sapien
8	317	12.8	415	1	TNR3_MOUSE	P50284 mus musculu
9	305	12.4	616	1	TR11_HUMAN	Q9y6q6 homo sapien
10	292.5	11.9	625	1	TR11_MOUSE	O35305 mus musculu
11	259	10.5	283	1	TR14_HUMAN	Q92956 homo sapien
12	252.5	10.2	289	1	TNR5_MOUSE	P27512 mus musculu
13	251.5	10.2	416	1	TR16_CHICK	P18519 gallus gall
14	242.5	9.8	269	1	TNR5_BOVIN	Q28203 bos taurus
15	241	9.8	595	1	TNR8_HUMAN	P28908 homo sapien
16	229.5	9.3	271	1	TNR4_RAT	P15725 rattus norv
17	223.5	9.1	272	1	TNR4_MOUSE	P47741 mus musculu
18	217	8.8	277	1	TNR4_HUMAN	P43489 homo sapien
19	210	8.5	427	1	TR16_HUMAN	P08138 homo sapien
20	199	8.1	471	1	TR1A_BOVIN	O19131 bos taurus
21	198	8.0	461	1	TR1A_PIG	P50555 sus scrofa
22	197	8.0	256	1	TNR9_MOUSE	P20334 mus musculu
23	197	8.0	425	1	TR16_RAT	P07174 rattus norv
24	191.5	7.8	454	1	TR1A_MOUSE	P25118 mus musculu
25	185.5	7.5	461	1	TR1A_RAT	P22934 rattus norv
26	185	7.5	255	1	TNR9_HUMAN	Q07011 homo sapien
27	183.5	7.4	455	1	TR1A_HUMAN	P19438 homo sapien
28	172	7.0	440	1	T10B_HUMAN	O14763 homo sapien
29	169.5	6.9	259	1	T10C_HUMAN	O14798 h tumor nec
30	166.5	6.7	1367	1	AMYH_YEAST	P08640 saccharomyc
31	153.5	6.2	830	1	SREC_HUMAN	Q14162 homo sapien
32	152	6.2	323	1	TNR6_BOVIN	P51867 bos taurus
33	148	6.0	327	1	TNR6_MOUSE	P25446 mus musculu
34	148	6.0	1210	1	PER3_HUMAN	P56645 homo sapien
35	147	6.0	600	1	SP96_DICDI	P14328 dictyosteli
36	146.5	5.9	687	1	VS41_GIALA	P92127 giardia lam
37	144.5	5.9	835	1	CD97_HUMAN	P48960 homo sapien
38	144	5.8	332	1	TNR6_PIG	O77736 sus scrofa
39	143.5	5.8	324	1	TNR6_RAT	Q63199 rattus norv
40	142	5.8	723	1	DLL1_HUMAN	O00548 homo sapien
41	141.5	5.7	335	1	TNR6_HUMAN	P25445 homo sapien
42	141.5	5.7	685	1	DLL4_HUMAN	Q9nr61 homo sapien
43	141.5	5.7	1113	1	PER3_MOUSE	O70361 mus musculu
44	141.5	5.7	3695	1	LMA5_HUMAN	O15230 homo sapien
45	141	5.7	1255	1	MUC1_HUMAN	P15941 h mucin 1 p

ALIGNMENTS

RESULT 1
TR1B_HUMAN
ID TR1B_HUMAN STANDARD; PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor
DE binding protein 2) (TBPII) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).
GN TNFRSF1B OR TNFR2 OR TNFBR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

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RX   MEDLINE=91056048; PubMed=2173696;
RA   Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA   Brockhaus M.;
RT   "Purification and partial amino acid sequence analysis of two
RT   distinct tumor necrosis factor receptors from HL60 cells.";
RL   J. Biol. Chem. 265:20131-20138(1990).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=93016040; PubMed=1328224;
RA   Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA   Lipari M.T., Goeddel D.V.;
RT   "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT   Characterization of ligand binding, internalization, and receptor
RT   phosphorylation.";
RL   J. Biol. Chem. 267:21172-21178(1992).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP   TRAF2.
RX   MEDLINE=99221490; PubMed=10206649;
RA   Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT   "Structural basis for self-association and receptor recognition of
RT   human TRAF2.";
RL   Nature 398:533-538(1999).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
CC       APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC       LEVEL ON THREONINE RESIDUES.
CC   -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC       Wyeth-Ayerst). Used to treat moderate to servere rheumatoid
CC       arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC       portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to
CC       TNF-alpha and blocks its interactions with receptors.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC   -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC       WWW="http://www.enbrelinfo.com/".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   ---------------------------------------------------------------------
DR   EMBL; M32315; AAA59929.1; -.
DR   EMBL; M35857; AAA63262.1; -.
DR   EMBL; U52165; AAC50622.1; -.
DR   EMBL; U52156; AAC50622.1; JOINED.
DR   EMBL; U52157; AAC50622.1; JOINED.
DR   EMBL; U52158; AAC50622.1; JOINED.
DR   EMBL; U52159; AAC50622.1; JOINED.
DR   EMBL; U52160; AAC50622.1; JOINED.
DR   EMBL; U52161; AAC50622.1; JOINED.
DR   EMBL; U52162; AAC50622.1; JOINED.
DR   EMBL; U52163; AAC50622.1; JOINED.
DR   EMBL; U52164; AAC50622.1; JOINED.
DR   EMBL; M55994; AAA36755.1; -.
DR   PIR; A35356; A35356.
DR   PIR; A36007; A36007.
DR   PIR; A36475; A36475.
DR   PIR; B35010; B35010.
DR   PIR; A23666; A23666.
DR   PDB; 1CA9; 12-APR-99.
DR   MIM; 191191; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Phosphorylation; Pharmaceutical; 3D-structure.
FT   SIGNAL       1    22
FT   CHAIN       23   461       TUMOR NECROSIS FACTOR RECEPTOR 2.
FT   DOMAIN      23   257       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   258   287       POTENTIAL.
FT   DOMAIN     288   461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      39    76       TNFR-CYS 1.
FT   REPEAT      77   118       TNFR-CYS 2.
FT   REPEAT     119   162       TNFR-CYS 3.
FT   REPEAT     163   201       TNFR-CYS 4.
FT   DISULFID    40    53       BY SIMILARITY.
FT   DISULFID    54    67       BY SIMILARITY.
FT   DISULFID    57    75       BY SIMILARITY.
FT   DISULFID    78    93       BY SIMILARITY.
FT   DISULFID    96   110       BY SIMILARITY.
FT   DISULFID   100   118       BY SIMILARITY.
FT   DISULFID   120   126       BY SIMILARITY.
FT   DISULFID   134   143       BY SIMILARITY.
FT   DISULFID   137   161       BY SIMILARITY.
FT   DISULFID   164   179       BY SIMILARITY.
FT   CARBOHYD   171   171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   193   193       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   141   141       R -> P (IN REF. 4).
FT   CONFLICT   196   196       R -> M (IN REF. 1 AND 3).
FT   CONFLICT   363   363       A -> T (IN REF. 4).
SQ   SEQUENCE   461 AA;  48316 MW;  603B580ECD67636F CRC64;


  Query Match             99.8%;  Score 2462;  DB 1;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-137;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     181 PHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||||
Db     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461


RESULT   2
TR1B_MOUSE
ID   TR1B_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
```

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DE   Tumor necrosis factor receptor 2 precursor (TNF-R2) (p75).
GN   TNFRSF1B OR TNFR2 OR TNFR-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    474       TUMOR NECROSIS FACTOR RECEPTOR 2.
FT   DOMAIN      23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   259    288       POTENTIAL.
FT   DOMAIN     289    474       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      39     77       TNFR-CYS 1.
FT   REPEAT      78    119       TNFR-CYS 2.
FT   REPEAT     120    164       TNFR-CYS 3.
FT   REPEAT     165    203       TNFR-CYS 4.
FT   DISULFID    40     54       BY SIMILARITY.
FT   DISULFID    55     68       BY SIMILARITY.
FT   DISULFID    58     76       BY SIMILARITY.
FT   DISULFID    79     94       BY SIMILARITY.
FT   DISULFID    97    111       BY SIMILARITY.
FT   DISULFID   101    119       BY SIMILARITY.
FT   DISULFID   121    127       BY SIMILARITY.
FT   DISULFID   136    145       BY SIMILARITY.
FT   DISULFID   139    163       BY SIMILARITY.
FT   DISULFID   166    181       BY SIMILARITY.
FT   CARBOHYD    69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462EAE398C4D6563 CRC64;


  Query Match             61.3%;  Score 1512;  DB 1;  Length 474;
  Best Local Similarity   63.0%;  Pred. No. 6.3e-82;
  Matches  293;  Conservative   50;  Mismatches  114;  Indels    8;  Gaps    6;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
           ||| |:| ||   |:|||  | :||||  ||| ||||  |:: :|||||: |||||:|| |
Db       1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy      60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
           ||: | || |||||||  || | |||:||    |||| | |::|||| :|||::|||:|
Db      61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120

Qy     120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
           |  | ||||    | || |  | || ||||||       :|:|| |||||||:|||||||:
Db     121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180

Qy     179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
           ||||:||:::|||||||  ||||   ||| |  |  ::: ||  ||||     | ||  |
Db     181 CRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP- 239

Qy     239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
             | |  :| :|  | || |  :||:||||||:||||::|:|||:|: | |||| ||||:
Db     240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQRKKKPSCLQRD 298

Qy     298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
           |||||:| :|::   | |||||| |||||||||||||||| |||||    |||  : ||
Db     299 AKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQ 358

Qy     357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
           |  |||||:  |||| | ||| |||||||||||||||||||||||:|:|| |: || ||
Db     359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 418

Qy     417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           ||||||||:|||  :|  || |||   : ||||||||||| |||||
Db     419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461


RESULT   3
VC22_VARV
ID   VC22_VARV      STANDARD;      PRT;   349 AA.
AC   P34015;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein C22/B28 homolog.
GN   G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=INDIA-1967 / ISOLATE IND3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Repeat.
FT   REPEAT       31     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;


  Query Match             15.4%;  Score 379.5;  DB 1;  Length 349;
  Best Local Similarity   37.6%;  Pred. No. 8.1e-16;
  Matches   79;  Conservative   24;  Mismatches   86;  Indels   21;  Gaps    7;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           || | |   |:  ||  :   :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PYTP-PNGKCKDTEY--KRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | ||||  ||:|:||||::|    |||| | ||:|| |    ||: |    ||  |:||:
Db      81 PACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNA--SMDAVCT-----ST 203
             |   ||:| ||  ||:|:| || | | |        :| |    :|   |      |
Db     141 -GHTSVGDVICSPCGFGTYSHTVSSADKCEP--------VPNNTFNYIDVEITLYPVNDT 191

Qy     204 SPTRSMAPGAVH--LPQPVSTRSQHTQPTP 231
           | ||:   |     |   ::    ||   |
Db     192 SCTRTTTTGLSESILTSELTITMNHTDCNP 221


RESULT   4
VT2_MYXVL
ID   VT2_MYXVL      STANDARD;      PRT;   326 AA.
AC   P29825;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor soluble receptor precursor (Protein T2).
GN   T2.
OS   Myxoma virus (strain Lausanne).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=31530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91335768; PubMed=1651597;
RA   Upton C., Macen J.L., Schreiber M., McFadden G.;
RT   "Myxoma virus expresses a secreted protein with homology to the tumor
RT   necrosis factor receptor gene family that contributes to viral
RT   virulence.";
RL   Virology 184:370-382(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M95181; AAA46632.1; -.
DR   EMBL; A23729; CAA01688.1; -.
DR   PIR; A40566; GQVZML.
DR   HSSP; P19438; 1TNR.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    326       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   REPEAT       27     62       TNFR-CYS 1.
FT   REPEAT       63    104       TNFR-CYS 2.
FT   REPEAT      105    147       TNFR-CYS 3.
FT   REPEAT      148    186       TNFR-CYS 4.
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   326 AA;  35208 MW;  ABBF027E947292FF CRC64;


  Query Match             14.6%;  Score 360.5;  DB 1;  Length 326;
  Best Local Similarity   36.9%;  Pred. No. 9.8e-15;
  Matches   75;  Conservative   29;  Mismatches   86;  Indels   13;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           ||  : |  ||  :|  :   :||: | || :|   |   |||||  |:: |:|   |
Db      20 PYGADRGK-CRGNDY--EKDGLCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHA 76

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | |:||  ||:    |:|:| : ::|:| |  | || |  |||||:|||  ||  |:||:
Db      77 PACVSCRGRCTGHLSESQSCDKTRDRVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYGVS 136

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN--ASMDAVCTSTSPTRS 208
             | | ||:|  |   |:|:  |||: |      | :::  |     |  ||:|:
Db     137 -GHTRTGDVLCTKCPRYTYSDAVSSTETCT--SSFNYISVEFNLYPVNDTSCTTTA---- 189

Qy     209 MAPGAVHLPQPVSTRSQHTQPTP 231
           |  |      |    ||   |
Db     190 -GPNEVVKTSEFSVTLNHTDCDP 211


RESULT   5
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lymphotoxin-beta receptor precursor (Tumor necrosis factor receptor
DE   2 related protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFCR OR TNFRSF3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
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RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 600979; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    435       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN       31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    248       POTENTIAL.
FT   DOMAIN      249    435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    168       TNFR-CYS 3.
FT   REPEAT      169    211       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    148       BY SIMILARITY.
FT   DISULFID    142    167       BY SIMILARITY.
FT   DISULFID    170    185       BY SIMILARITY.
FT   CARBOHYD     40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;


  Query Match             13.8%;  Score 341.5;  DB 1;  Length 435;
  Best Local Similarity   29.1%;  Pred. No. 1.7e-13;
  Matches  120;  Conservative   45;  Mismatches  141;  Indels  107;  Gaps   25;

Qy       2 APVAVWAALAVGL-ELWAAA--HALPAQVAFTPYAPEPGSTCR--LREYYDQTAQMCCSK 56
           ||   |  | :||  | ||:   |:|      ||| |   |||   :|||:   ::|||:
Db       9 APGLAWGPLVLGLFGLLAASQPQAVP------PYASE-NQTCRDQEKEYYEPQHRICCSR 61

Qy      57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQV----ETQACTR 112
           | || :    |::  |||| :| :::| : ||::  |  |       | |    |   ||
Db      62 CPPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCR---PCDPVMGLEEIAPCTS 118

Qy     113 EQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVV------CKPCAP 166
           ::   | |:|| :||    | |  |  |  | ||       |  | |      | ||
Db     119 KRKTQCRCQPGMFCAAWALE-CTHCELLSDCPPG-----TEAELKDEVGKGNNHCVPCKA 172

Qy     167 GTFSNTTSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPG--------AV 214
           | | ||:| :  |:||  |      | | || | |  |   :|   : |          ||
Db     173 GHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPPEMSGTMLMLAV 230

Qy     215 HLPQP----VST------RSQHTQPTPEPSTAPSTSFLL---PMGPSP-PAEGS------ 254
             ||      ::|      :|        ||       ||   | |  | |  ||
Db     231 LLPLAFFLLLATVFSCIWKS-------HPSLCRKLGSLLKRRPQGEGPNPVAGSWEPPKA 283

Qy     255 -------------TGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
                      :|| : ||    |: |  :|  ||          :: || | ||
Db     284 HPYFPDLVQPLLPISGDVS-PVS--TGLPAAPVLEAGVPQ-------QQSPLDLTRE--- 330

Qy     301 PHL-PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPG 352
           | | | ::::   |    |:       :  |:  : :       |    |  ||
Db     331 PQLEPGEQSQVAHGTNGIHV-------TGGSMTITGNIYIYNGPVLGGPPGPG 376


RESULT   6
VT2_SFVKA
ID   VT2_SFVKA      STANDARD;      PRT;   325 AA.
AC   P25943;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor soluble receptor precursor (Protein T2).
GN   T2.
OS   Shope fibroma virus (strain Kasza) (SFV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
OX   NCBI_TaxID=10272;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87321103; PubMed=2820128;
RA   Upton C., Delange A.M., McFadden G.;
RT   "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT   telomeric region of the Shope fibroma virus genome.";
RL   Virology 160:20-30(1987).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=91207415; PubMed=1850261;
RA   Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA   McFadden G., Goodwin R.G.;
RT   "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT   form of the TNF receptor.";
RL   Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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CC   ---------------------------------------------------------------------
DR   EMBL; M17433; -; NOT_ANNOTATED_CDS.
DR   EMBL; A23727; CAA01687.1; -.
DR   PIR; B43692; B43692.
DR   HSSP; P19438; 1EXT.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    325       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   REPEAT       27     62       TNFR-CYS 1.
FT   REPEAT       63    104       TNFR-CYS 2.
FT   REPEAT      105    147       TNFR-CYS 3.
FT   REPEAT      148    186       TNFR-CYS 4.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT   CARBOHYD    205    205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    238    238       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   325 AA;  35132 MW;  810530339198A71E CRC64;


  Query Match           13.3%;  Score 328;  DB 1;  Length 325;
  Best Local Similarity   36.9%;  Pred. No. 7.8e-13;
  Matches   66;  Conservative   28;  Mismatches   71;  Indels   14;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           ||:   |  |   :|  :   :||: | || :|   |   |:|||  ||| |:|   |
Db      20 PYSSNQGK-CGGHDY--EKDGLCCASCHPGFYASRLCGPGSNTVCSPCEDGTFTASTNHA 76

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
           | |:||   |:    |:| | |  :|:| |  | || |  | |||:|||  ||  |:||:
Db      77 PACVSCRGPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQNGCRICAPQTKCPAGYGVS 136

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI-----PGNASMDAVCTSTS 204
             |   | :|: | | |:|:: | |: |      | :::     | |   :  ||:|:
Db     137 -GHTRAGDTLCEKCPPHTYSDSLSPTERCGTS--FNYISVGFNLYPVN---ETSCTTTA 189


RESULT   7
TNR5_HUMAN
ID   TNR5_HUMAN     STANDARD;      PRT;   277 AA.
AC   P25942;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 5 precursor
DE   (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).
GN   TNFRSF5 OR CD40.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89356608; PubMed=2475341;
RA   Stamenkovic I., Clark E.A., Seed B.;
RT   "A B-lymphocyte activation molecule related to the nerve growth
RT   factor receptor and induced by cytokines in carcinomas.";
RL   EMBO J. 8:1403-1410(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [3]
RP   3D-STRUCTURE MODELING OF 24-144.
RX   MEDLINE=97189482; PubMed=9037712;
RA   Bajorath J., Aruffo A.;
RT   "Construction and analysis of a detailed three-dimensional model of
RT   the ligand binding domain of the human B cell receptor CD40.";
RL   Proteins 27:59-70(1997).
RN   [4]
RP   3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX   MEDLINE=98266353; PubMed=9605317;
RA   Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M.,
RA   Zheng Z., Naismith J.H., Thomas D.;
RT   "The role of polar interactions in the molecular recognition of CD40L
RT   with its receptor CD40.";
RL   Protein Sci. 7:1124-1135(1998).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X60592; CAA43045.1; -.
DR   EMBL; AL035662; CAC17670.1; -.
DR   PIR; S04460; S04460.
DR   PDB; 1CDF; 01-APR-97.
DR   MIM; 109535; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW   3D-structure.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    277       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 5.
FT   DOMAIN      20    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   194    215       POTENTIAL.
FT   DOMAIN     216    277       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      25     60       TNFR-CYS 1.
FT   REPEAT      61    103       TNFR-CYS 2.
FT   REPEAT     104    144       TNFR-CYS 3.
FT   REPEAT     145    187       TNFR-CYS 4.
FT   DISULFID    26     37
FT   DISULFID    38     51
FT   DISULFID    41     59
FT   DISULFID    62     77
FT   DISULFID    83    103
FT   DISULFID   105    119
FT   DISULFID   111    116
FT   DISULFID   125    143
FT   CARBOHYD   153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   277 AA;  30619 MW;  BC8776EC2C4A5680 CRC64;


  Query Match           12.9%;  Score 317.5;  DB 1;  Length 277;
  Best Local Similarity   26.7%;  Pred. No. 2.7e-12;
  Matches   92;  Conservative   32;  Mismatches  124;  Indels   97;  Gaps   11;

Qy      23 LPAQVA-----FTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS 77
           || |         |   ||| : || ::|   :   ||| | |||     ||: ::| |
Db       4 LPLQCVLWGCLLTAVHPEPPTACREKQYLINS--QCCSLCQPGQKLVSDCTEFTETECLP 61
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Qy      78 CEDSTYTQLWNWVPEC-------LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
Db      62 CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ------QKGTSETDTICTCEEGWHCT--- 112

Qy     131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN---- 186
Db     113 SEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDL 172

Qy     187 VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMG 246
Db     173 VVQQAGTNKTDVVCGPQDRLRAL---------------------------------- 195

Qy     247 PSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPH---- 302
Db     196 -------------VVIPIIFGILFAILLVL-----VFIKKVAKKP-----TNKAPHPKQE 232

Qy     303 -----LPAD-KARGTQGPEQQHLLITAPSSSSSSLESSASALDRR 341
Db     233 PQEINFPDDLPGSNTAAPVQETLHGCQPVTQEDGKESRISVQERQ 277


RESULT   8
TNR3_MOUSE
ID   TNR3_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lymphotoxin-beta receptor precursor.
GN   LTBR OR TNFCR OR TNFRSF3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    415       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN      31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   224    244       POTENTIAL.
FT   DOMAIN     245    415       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    170       TNFR-CYS 3.
FT   REPEAT     171    213       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    150       BY SIMILARITY.
FT   DISULFID   142    169       BY SIMILARITY.
FT   DISULFID   172    187       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;


  Query Match             12.8%;  Score 317;  DB 1;  Length 415;
  Best Local Similarity   24.9%;  Pred. No. 4.3e-12;
  Matches  119;  Conservative   50;  Mismatches  166;  Indels  142;  Gaps   22;

Qy       7 WAALAVGLELWAAAHALPAQVAFTPYAPEPGSTC--RLREYYDQTAQMCCSKCSPGQHAK 64
Db      14 WGPLLLGLSGLLVA-SQPQLV--PPYRIE-NQTCWDQDKEYYEPMHDVCCSRCPPGEFVF 69

Qy      65 VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQV----ETQACTREQNRICTC 120
Db      70 AVCSRSQDTVCKTCPHNSYNEHWNHLSTCQLCR---PCDIVLGFEEVAPCTSDRKAECRC 126

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTET--------SDVVCKPCAPGTFSNT 172
Db     127 QPGMSCVYLDNE-CVHCEEER-----LVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNT 180

Qy     173 TSSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQ 228
Db     181 SSPRARCQPHTRCEIQGLVEAAPGTSYSDTICKN-------------------------- 214

Qy     229 PTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIM---- 284
Db     215 -PPEPGAMLLLAILLSL-----------------------VLFLLFTTVLACAWMRHPS 249

Qy     285 ------TQVKK------KPLCLQREAKVPHLP----------ADKARGTQGPEQQHLLIT 322
Db     250 LCRKLGTLLKRHPEGEESPPCPAPRAD-PHFPDLAEPLLPMSGDLSPSPAGPP------T 302

Qy     323 APSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVT 382
Db     303 APSLEEVVLQQQSPLV----------QARELEAEPGEHGQVAHGAN----GIHVTGGSVT 348

Qy     383 CIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPF--SKEECAFRSQLETP 437
Db     349 VTGNIYIYN----------GPVLGGT-RGPGDPPAPPEPPYPTPEEGAPGPSELSTP 394


RESULT   9
TR11_HUMAN
ID   TR11_HUMAN     STANDARD;      PRT;   616 AA.
AC   Q9Y6Q6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11A precursor
DE   (Receptor activator of NF-KB) (Osteoclast differentiation factor
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DE   receptor) (ODFR).
GN   TNFRSF11A OR RANK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=99097247; PubMed=9878548;
RA   Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA   Morinaga T., Higashio K.;
RT   "RANK is the essential signaling receptor for osteoclast
RT   differentiation factor in osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN   [3]
RP   VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
RP   V-192.
RX   MEDLINE=20082806; PubMed=10615125;
RA   Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA   Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA   Anderson D.M.;
RT   "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT   familial expansile osteolysis.";
RL   Nat. Genet. 24:45-48(2000).
CC   -!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC       OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
CC       MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC       INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC       SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC       GLAND.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
CC       OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC       CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC       OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC       ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
CC       LOSS OF DENTITION.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
CC       DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
CC       IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
CC       UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
CC       AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF018253; AAB86809.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 603499; -.
DR   MIM; 174810; -.
DR   MIM; 602080; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Glycoprotein; Transmembrane; Repeat; Signal; Polymorphism;
KW   Disease mutation.
FT   SIGNAL       1     29       POTENTIAL.
FT   CHAIN       30    616       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 11A.
FT   DOMAIN      30    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   213    233       POTENTIAL.
FT   DOMAIN     234    616       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      34     68       TNFR-CYS 1.
FT   REPEAT      71    112       TNFR-CYS 2.
FT   REPEAT     114    151       TNFR-CYS 3.
FT   REPEAT     154    194       TNFR-CYS 4.
FT   DISULFID    34     46       BY SIMILARITY.
FT   DISULFID    47     60       BY SIMILARITY.
FT   DISULFID    50     68       BY SIMILARITY.
FT   DISULFID    71     86       BY SIMILARITY.
FT   DISULFID    92    112       BY SIMILARITY.
FT   DISULFID   114    127       BY SIMILARITY.
FT   DISULFID   133    151       BY SIMILARITY.
FT   CARBOHYD   105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     13     21       ALLLLCALL -> ALLLLCALLALLLLCALL (IN
FT                               PDB2).
FT                               /FTId=VAR_011516.
FT   VARIANT     16     21       LLCALL -> LLCALLLLCALL (IN FEO).
FT                               /FTId=VAR_011517.
FT   VARIANT    192    192       A -> V.
FT                               /FTId=VAR_011518.
SQ   SEQUENCE   616 AA;  66033 MW;  E3DE9A7A08196F81 CRC64;
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Query Match 12.4%; Score 305; DB 1; Length 616;
Best Local Similarity 22.4%; Pred. No. 3.2e-11;
Matches 125; Conservative 48; Mismatches 187; Indels 198; Gaps 20;

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Qy       5 AVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAK 64
           |: | | | |::                ||     |   ::|:   : ||:|| ||::
Db      19 ALLARLQVALQI----------------AP----PCTSEKHYEHLGR-CCNKCEPGKYMS 57

Qy      65 VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQ--VETQACTREQNRICTCRP 122
             || |||:||  |    |   ||   :||     | : :  |   |      | | |
Db      58 SKCTTTSDSVCLPCGPDEYLDSWNEEDKCL-LHKVCDTGKALVAVVAGNSTTPRRCACTA 116

Qy     123 GWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPH 182
           |:: :    : |  |    :| || |   |     | |||||  | ||:  |||| |||
Db     117 GYHWS----QDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFSSTDKCRPW 172

Qy     183 QICNV----VAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPST-AP 237
           |      |   |    ||||:|: | |                    :|  ||    |
Db     173 TNCTFLGKRVEHHGTEKSDAVCSSSLPAR-------------------KPPNEPHVYLP 212

Qy     238 STSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
             ||                   |   |  :  :| ||              | :::
Db     213 GLIILL-------------------LFASVALVAAIIFGV-------------CYRKK 238

Qy     298 AKV-------------PHLPADKAR------------GTQGPEQQHLLITAPSS----- 326
           |               |  ||              | ||  :  ||:|
Db     239 GKALTANLWHWINEACGRLSGDKESSGDSCVSTHTANFGQQGACEGVLLLTLEEKTFPED 298

Qy     327 --------------------------------SSSSLESSASALDRRAPTRNQ----PQA 350
                                          | : :|  :    |: || ::    |
Db     299 MCYPDQGGVCQGTCVGGGPYAQGEDARMLSLVSKTEIEEDSF---RQMPTEDEYMDRPSQ 355

Qy     351 PGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGD--- 407
           |  :     |     ||  : |     :|          :|  |||  :   ||:|
Db     356 PTDQLLFLTE----PGSKSTPPFSEPLEV---------GENDSLSQCFTGTQSTVGSESC 402

Qy     408 --------TDSSPSESPKDEQVPFSKEECAFRSQLETP----------------ETLLG 442
                 || :|  |    |       |   :  :|                  | |:|
Db     403 NCTEPLCRTDWTPMSSENYLQKEVDSGHCPHWAASPSPNWADVCTGCRNPPGEDCEPLVG 462

Qy     443 STEEKPLPLGVPDAGMKP 460
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          | :  |||      |: |
Db    463 SPKRGPLPQCAYGMGLPP 480


RESULT  10
TR11_MOUSE
ID   TR11_MOUSE     STANDARD;      PRT;   625 AA.
AC   O35305;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11A precursor
DE   (Receptor activator of NF-KB) (Osteoclast differentiation factor
DE   receptor) (ODFR).
GN   TNFRSF11A OR RANK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=99097247; PubMed=9878548;
RA   Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA   Morinaga T., Higashio K.;
RT   "RANK is the essential signaling receptor for osteoclast
RT   differentiation factor in osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC   -!- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC       OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
CC       MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC       INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC       TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC       WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF019046; AAB86810.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:1314891; Tnfrsf11a.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    625       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11A.
FT   DOMAIN       31    214       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    215    234       POTENTIAL.
FT   DOMAIN      235    625       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       35     69       TNFR-CYS 1.
FT   REPEAT       72    113       TNFR-CYS 2.
FT   REPEAT      115    152       TNFR-CYS 3.
FT   REPEAT      155    195       TNFR-CYS 4.
FT   DISULFID     35     47       BY SIMILARITY.
FT   DISULFID     48     61       BY SIMILARITY.
FT   DISULFID     51     69       BY SIMILARITY.
FT   DISULFID     72     87       BY SIMILARITY.
FT   DISULFID     93    113       BY SIMILARITY.
FT   DISULFID    115    128       BY SIMILARITY.
FT   DISULFID    134    152       BY SIMILARITY.
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    175    175       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   625 AA;  66621 MW;  F8C1872E99511D8E CRC64;


  Query Match             11.9%;  Score 292.5;  DB 1;  Length 625;
  Best Local Similarity   23.1%;  Pred. No. 1.7e-10;
  Matches  123;  Conservative   50;  Mismatches  197;  Indels  163;  Gaps   22;

Qy      23 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82
           :| ||       |     |    :|:   : |||:| ||::    || |||:||  |
Db      23 VPLQVTLQVTPP-----CTQERHYEHLGR-CCSRCEPGKYLSSKCTPTSDSVCLPCGPDE 76

Qy      83 YTQLWNWVPECLSCGSRCSSDQ--VETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL 140
           |   ||   :||     | : :  |          | | |  |::          |  |
Db      77 YLDTWNEEDKCL-LHKVCDAGKALVAVDPGNHTAPRRCACTAGYHW----NSDCECCRRN 131

Qy     141 RKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVV----AIPGNASM 196
           :| |||    |     | || ||  | ||:  |||| |:|   | ::    |  |
Db     132 TECAPGFGAQHPLQLNKDTVCTPCLLGFFSDVFSSTDKCKPWTNCTLLGKLEAHQGTTES 191

Qy     197 DAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 256
           | ||:|:   |                |    :  ||   ||
Db     192 DVVCSSSMTLR------------------RPPKEAQAYLPSLIVLL------------- 219

Qy     257 DFALPVGLIVGVTALGLLIIGV----------------VN--CVIMTQVKKKP------- 291
                 | : |  :  :| ||                ||  |  ::  |:
Db     220 -------LFISVVVVAAIIFGVYYRKGGKALTANLWNWVNDACSSLSGNKESSGDRCAGS 272

Qy     292 --------------LCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSAS- 336
                          | : || |:  :| | | |  ||      : |     : :  | :
Db     273 HSATSSQQEVCEGILLMTREEKM--VPEDGA-GVCGP------VCAAGGPWAEVRDSRTF 323

Qy     337 ----------ALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVN 386
                      | |: || ::      : |          ||     |     :|
Db     324 TLVSEVETQGDLSRKIPTEDEYTDRPSQPSTGSLLLIQQGSKSIPPFQEPLEV------- 376

Qy     387 VCSSSDHSSQCSSQASSTMGD-----------TDSSPSESPK--------DEQVPF---S 424
               :| ||| :   ||:              ||| |    |         |  :|:  |
Db     377 --GENDSLSQCFTGTESTVDSEGCDFTEPPSRTDSMPVSPEKHLTKEIEGDSCLPWVVSS 434

Qy     425 KEECAFRSQLETP----ETLLGSTEEKPLP-----LGVP--------DAGMKP 460
           :     ||    |   || : |||     :| |        :||::|
Db     435 NSTDGYTGSGNTPGEDHEPFPGSLKCGPLPQCAYSMGFPSEAAASMAEAGVRP 487


RESULT  11
TR14_HUMAN
ID   TR14_HUMAN     STANDARD;      PRT;   283 AA.
AC   Q92956; Q9UM65;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor
DE   (Herpesvirus entry mediator) (Tumor necrosis factor receptor-like 2)
DE   (TR2).
GN   TNFRSF14 OR HVEM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervical adenocarcinoma;
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RX   MEDLINE=97053782; PubMed=8898196;
RA   Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT   "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT   the TNF/NGF receptor family.";
RL   Cell 87:427-436(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97306336; PubMed=9162061;
RA   Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA   Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA   Porter T.G., Truneh A., Young P.R.;
RT   "A newly identified member of the tumor necrosis factor receptor
RT   superfamily with a wide tissue distribution and involvement in
RT   lymphocyte activation.";
RL   J. Biol. Chem. 272:14272-14276(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Zhang W., Wan T., Cao X.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
CC       PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED
CC       THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OF BOTH SEROTYPES INTO
CC       CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC       IN LUNG, SPLEEN, AND THYMUS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U70321; AAB58354.1; -.
DR   EMBL; U81232; AAD00505.1; -.
DR   EMBL; AF153978; AAF75588.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 602746; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     38       POTENTIAL.
FT   CHAIN       39    283       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 14.
FT   DOMAIN      39    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   203    223       POTENTIAL.
FT   DOMAIN     224    283       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     75       TNFR-CYS 1.
FT   REPEAT      78    119       TNFR-CYS 2.
FT   REPEAT     121    162       TNFR-CYS 3.
FT   DISULFID    42     53       BY SIMILARITY.
FT   DISULFID    54     67       BY SIMILARITY.
FT   DISULFID    57     75       BY SIMILARITY.
FT   DISULFID    78     93       BY SIMILARITY.
FT   DISULFID    96    111       BY SIMILARITY.
FT   DISULFID    99    119       BY SIMILARITY.
FT   DISULFID   121    127       BY SIMILARITY.
FT   DISULFID   138    162       BY SIMILARITY.
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    17     17       K -> R (IN REF. 1).
SQ   SEQUENCE   283 AA;  30392 MW;  46CE13C2C70242C1 CRC64;

  Query Match          10.5%;  Score 259;  DB 1;  Length 283;
  Best Local Similarity  32.8%;  Pred. No. 7.4e-09;
    Matches   59;  Conservative   23;  Mismatches   76;  Indels   22;  Gaps    6;

Qy      32 YAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVP 91
           |||   | |:  ||       || |||||   |  | : : |||: |   ||    | :
Db      35 YAPALPS-CKEDEY--PVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLS 91

Qy      92 ECLSC-------GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCR 144
           :|| |       | | | :      |:| :| :| | || :| :   : |  |
Db      92 KCLQCQMCDPAMGLRASRN------CSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSS 145

Qy     145 PGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTS 204
           ||  | : |||: | :|: | |||||    : : |:    |: :     |      ||:|
Db     146 PGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKCSWLVTKAGAG-----TSSS 199


RESULT  12
TNR5_MOUSE
ID   TNR5_MOUSE     STANDARD;      PRT;   289 AA.
AC   P27512;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 5 precursor
DE   (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40).
GN   TNFRSF5 OR CD40.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92105763; PubMed=1370315;
RA   Torres R.M., Clark E.A.;
RT   "Differential increase of an alternatively polyadenylated mRNA
RT   species of murine CD40 upon B lymphocyte activation.";
RL   J. Immunol. 148:620-626(1992).
RN   [2]
RP   REVISIONS.
RC   STRAIN=BALB/C;
RA   Torres R.M.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Liver;
RX   MEDLINE=93094586; PubMed=1281194;
RA   Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA   Howard M., Cockayne D.A.;
RT   "Genomic structure and chromosomal mapping of the murine CD40 gene.";
RL   J. Immunol. 149:3921-3926(1992).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   ---------------------------------------------------------------------
DR   EMBL; M83312; AAB08705.1; -.
DR   EMBL; M94126; AAA37404.1; -.
DR   EMBL; M94129; AAA37404.1; JOINED.
DR   EMBL; M94128; AAA37404.1; JOINED.
DR   EMBL; M94127; AAA37404.1; JOINED.
DR   PIR; A46476; A46476.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:88336; Tnfrsf5.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
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DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    289       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 5.
FT   DOMAIN       20    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    215       POTENTIAL.
FT   DOMAIN      216    289       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       25     60       TNFR-CYS 1.
FT   REPEAT       61    103       TNFR-CYS 2.
FT   REPEAT      104    144       TNFR-CYS 3.
FT   REPEAT      145    187       TNFR-CYS 4.
FT   DISULFID     26     37       BY SIMILARITY.
FT   DISULFID     38     51       BY SIMILARITY.
FT   DISULFID     41     59       BY SIMILARITY.
FT   DISULFID     62     77       BY SIMILARITY.
FT   DISULFID     83    103       BY SIMILARITY.
FT   DISULFID    105    119       BY SIMILARITY.
FT   DISULFID    111    116       BY SIMILARITY.
FT   DISULFID    125    143       BY SIMILARITY.
FT   CARBOHYD    153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   289 AA;  32111 MW;  C791CB6D2FEA574E CRC64;


  Query Match           10.2%;  Score 252.5;  DB 1;  Length 289;
  Best Local Similarity  22.5%;  Pred. No. 1.8e-08;
  Matches   80;  Conservative   38;  Mismatches  134;  Indels  103;  Gaps   12;

Qy       5 AVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAK 64
           |:|  |   : |                        ||  ::|       ||  | ||
Db       9 ALWGCLLTAVHLGQCV-----------------TCSDKQYLHD--GQCCDLCQPGSRLT 48

Qy      65 VFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQ---VETQACTREQNRICTCR 121
             ||    | |  |:   ::  ||    |      |  :|   |: :  | | : :|||:
Db      49 SHCTALEKTQCHPCDSGEFSAQWNREIRCHQ-HRHCEPNQGLRVKKEG-TAESDTVCTCK 106

Qy     122 PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRP 181
           | :|     : |  ||    | |||||    |||:| || ||  | ||| :|  : | |
Db     107 EGQHCT---SKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYP 163

Qy     182 HQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 237
           |     |   | :  : :|   |  |::
Db     164 WTSCEDKNLEVLQKGTSQTNVICGLKSRMRAL---------------------------- 195

Qy     238 STSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
                           :|| : : :|  |: :        : :| |||   :
Db     196 --------------------LVIPVVMGILITIFGVFL-------YIKKVVKKP---KDN 225

Qy     298 AKVPHLPADK----------ARGTQGPEQQHLLITAPSSSSSSLESSASALDRR 341
           :|  || :              |  | |: |    | :     ||  |  :|:
Db     226 EMLP--PAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQ 278


RESULT  13
TR16_CHICK
ID   TR16_CHICK     STANDARD;      PRT;   416 AA.
AC   P18519;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE   affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE   (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN   NGFR OR TNFRSF16.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=90166579; PubMed=2560385;
RA   Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
RA   Shooter E.M., Reichardt L.F.;
RT   "Structure and developmental expression of the nerve growth factor
RT   receptor in the chicken central nervous system.";
RL   Neuron 2:1123-1134(1989).
RN   [2]
RP   SEQUENCE OF 21-416 FROM N.A.
RX   MEDLINE=90152140; PubMed=2154393;
RA   Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
RT   "Structure and developmental expression of the chicken NGF receptor.";
RL   Dev. Biol. 137:287-304(1990).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
CC       AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF
CC       NEURAL CELLS (By similarity).
CC   -!- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
DR   PIR; JN0006; JN0006.
DR   PIR; A60504; A60504.
DR   HSSP; P07174; 1NGR.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal; Apoptosis.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    416       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 16.
FT   DOMAIN       29    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    240    261       POTENTIAL.
FT   DOMAIN      262    416       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       23     57       TNFR-CYS 1.
FT   REPEAT       58     99       TNFR-CYS 2.
FT   REPEAT      100    138       TNFR-CYS 3.
FT   REPEAT      140    180       TNFR-CYS 4.
FT   DOMAIN      333    410       DEATH.
FT   DOMAIN      188    236       SER/THR-RICH.
FT   DISULFID     24     35       BY SIMILARITY.
FT   DISULFID     36     49       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID     78     91       BY SIMILARITY.
FT   DISULFID     81     99       BY SIMILARITY.
FT   DISULFID    101    114       BY SIMILARITY.
FT   DISULFID    117    130       BY SIMILARITY.
FT   DISULFID    120    138       BY SIMILARITY.
FT   DISULFID    141    156       BY SIMILARITY.
FT   DISULFID    159    172       BY SIMILARITY.
FT   DISULFID    162    180       BY SIMILARITY.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     36     36       C -> Y (IN REF. 2).
FT   CONFLICT    173    173       T -> K (IN REF. 2).
FT   CONFLICT    276    276       N -> S (IN REF. 2).
FT   CONFLICT    396    396       K -> R (IN REF. 2).
SQ   SEQUENCE   416 AA;  44654 MW;  6BCEAAB54F4D2D56 CRC64;


  Query Match           10.2%;  Score 251.5;  DB 1;  Length 416;
  Best Local Similarity  25.1%;  Pred. No. 2.9e-08;
  Matches   89;  Conservative   48;  Mismatches  164;  Indels   53;  Gaps   16;

Qy      23 LPAQVAFTPYAPEPGS--TCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED 80
             :|  :   |  |  ||   |  : |   |:  ||  |: |:     |   : |||: | |
Db       5 VPLLLLLLPAGPTWGSKEKCLTKMY--TTSGECCKACNLGEGVVQPC-GVNQTVCEPCLD 61
```

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Qy      81 S-TYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAP 139
           | ||:   :    |  | ::|      :  |    : :| |  |::    : |    |
Db      62 SVTYSDTVSATEPCKPC-TQCVGLHSMSAPCVESDDAVCRCAYGYF----QDELSGSCKE 116

Qy     140 LRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAV 199
           |  |||:  |  :: | ||: |  ||||:  :  | | |  ||       |  |
Db     117 CSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANFVDPCLPCTICE-----ENEVMVKE 171

Qy     200 CTSTSPT--RSMAP-GAVHLPQPVSTRSQHTQPTPEP----------STAPSTSFLLPM 245
           ||:||    | : |    | |    : |      |||          :|  :      |
Db     172 CTATSDAECRDLHPRWTTHTPSLAGSDS------PEPITRDPFNTEGMATTLADIVTTVM 225

Qy     246 GPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLP 304
           | | |     | |  :||   :    |  :::|:|  :     |:   | | :    : |
Db     226 GSSQPVVSRGTADNLIPVYCSI----LAAVVVGLVAYIAF---KRWNSCKQNKQGANNRP 278

Qy     305 ADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGA 358
           ::   |  || : |       | | :   : :|  : |     | |  :  |:
Db     279 VNQ---TPSPEGEKL------HSDSGISVDSQSLHDQQPPNQSTQGPAPKGDGS 323


RESULT  14
TNR5_BOVIN
ID   TNR5_BOVIN     STANDARD;      PRT;   269 AA.
AC   Q28203;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 5 precursor
DE   (CD40L receptor) (B-cell surface antigen CD40) (Fragment).
GN   TNFRSF5 OR CD40.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97281252; PubMed=9135560;
RA   Hirano A., Brown W.C., Estes D.M.;
RT   "Cloning, expression and biological function of the bovine CD40
RT   homologue: role in B-lymphocyte growth and differentiation in
RT   cattle.";
RL   Immunology 90:294-300(1997).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57745; AAC48710.1; -.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20   >269       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 5.
FT   DOMAIN       20    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    215       POTENTIAL.
FT   DOMAIN      216   >269       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       25     60       TNFR-CYS 1.
FT   REPEAT       61    103       TNFR-CYS 2.
FT   REPEAT      104    144       TNFR-CYS 3.
FT   REPEAT      145    187       TNFR-CYS 4.
FT   DISULFID     26     37       BY SIMILARITY.
FT   DISULFID     38     51       BY SIMILARITY.
FT   DISULFID     41     59       BY SIMILARITY.
FT   DISULFID     62     77       BY SIMILARITY.
FT   DISULFID     83    103       BY SIMILARITY.
FT   DISULFID    105    119       BY SIMILARITY.
FT   DISULFID    111    116       BY SIMILARITY.
FT   DISULFID    125    143       BY SIMILARITY.
FT   CARBOHYD    153    153       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     269    269
SQ   SEQUENCE   269 AA;  29983 MW;  746903F30F95F387 CRC64;


  Query Match             9.8%;  Score 242.5;  DB 1;  Length 269;
  Best Local Similarity   31.0%;  Pred. No. 6.5e-08;
  Matches   63;  Conservative   17;  Mismatches   96;  Indels   27;  Gaps    6;

Qy      23 LPAQVAF-----TPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS 77
           || |  |     |    || : |  ::|      :||  | |||     ||: | | | |
Db       4 LPLQCLFWGFFLTAVHSEPATACGEKQY--PVNSLCCDLCPPGQKLVNDCTEVSKTECQS 61

Qy      78 CEDSTYTQLWNWVPEC-------LSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
           |    :   ||    |        : | |  |:       |   : || |  | :|
Db      62 CGKGEFLSTWNREKYCHEHRYCNPNLGLRIQSEG------TLNTDTICVCVEGQHCT--- 112

Qy     131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN---- 186
           |  | |   | ||||| :  |   | ||:||  | ||| :|: : |     |
Db     113 SHTCESCTPHSLCLPGFGVKQIATGLLDTVCEPCPLGFFSNVSSAFEKCHRWTSCERKGL 172

Qy     187 VVAIPGNASMDAVCTSTSPTRSM 209
           |    |    | ||   |  |::
Db     173 VEQHVGTNKTDVVCGFQSRMRTL 195


RESULT  15
TNR8_HUMAN
ID   TNR8_HUMAN     STANDARD;      PRT;   595 AA.
AC   P28908;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 8 precursor (CD30L
DE   receptor) (Lymphocyte activation antigen CD30) (KI-1 antigen).
GN   TNFRSF8 OR CD30.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoid;
RX   MEDLINE=92154659; PubMed=1310894;
RA   Duerkop H., Latza U., Hummel M., Eitelbach F., Seed B., Stein H.;
RT   "Molecular cloning and expression of a new member of the nerve growth
RT   factor receptor family that is characteristic for Hodgkin's
RT   disease.";
RL   Cell 68:421-427(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95089787; PubMed=7527901;
RA   Jung W., Krueger S., Renner C., Gause A., Sahin U., Trumper L.,
RA   Pfreundschuh M.;
RT   "Opposite effects of the CD30 ligand are not due to CD30 mutations:
RT   results from cDNA cloning and sequence comparison of the CD30 antigen
RT   from different sources.";
RL   Mol. Immunol. 31:1329-1334(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (VARIANT C30V).
RX   MEDLINE=96437016; PubMed=8839832;
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RA   Horie R., Ito K., Tatewaki M., Nagai M., Aizawa S.,
RA   Higashihara M., Ishida T., Inoue J., Takizawa H., Watanabe T.;
RT   "A variant CD30 protein lacking extracellular and transmembrane domain
RT   is induced in HL-60 by tetradecanoylphorbol acetate and is expressed
RT   in alveolar macrophages.";
RL   Blood 88:2422-2432(1996).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD30L. MAY PLAY
CC       A ROLE IN THE REGULATION OF CELLULAR GROWTH AND TRANSFORMATION OF
CC       ACTIVATED LYMPHOBLASTS. REGULATES GENE EXPRESSION THROUGH
CC       ACTIVATION OF NFKB.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: A SHORTER CYTOPLASMIC FORM (C30V) WHICH IS
CC       ONLY EXPRESSED IN ALVEOLAR MACROPHAGES IS PRODUCED BY THE USE
CC       OF AN ALTERNATIVE INITIATION CODON IN THE SAME READING FRAME.
CC   -!- PTM: PHOSPHORYLATED ON SERINE AND TYROSINE RESIDUES.
CC   -!- DISEASE: MOST SPECIFIC HODGKIN'S DISEASE ASSOCIATED ANTIGEN.
CC   -!- SIMILARITY: CONTAINS 6 TNFR-CYS REPEATS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD30 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd30.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M83554; AAA51947.1; -.
DR   EMBL; S75768; AAD14188.1; -.
DR   EMBL; D86042; BAA12973.1; -.
DR   PIR; A42086; A42086.
DR   HSSP; P19438; 1NCF.
DR   MIM; 153243; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW   Phosphorylation; Alternative initiation.
FT   SIGNAL        1     18
FT   CHAIN        19    595       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 8, LONG ISOFORM.
FT   CHAIN       464    595       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 8, SHORT ISOFORM.
FT   INIT_MET    464    464       FOR SHORT ISOFORM.
FT   DOMAIN       19    379       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    380    407       POTENTIAL.
FT   DOMAIN      408    595       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       28     66       TNFR-CYS 1.
FT   REPEAT       68    106       TNFR-CYS 2.
FT   REPEAT      107    150       TNFR-CYS 3.
FT   REPEAT      205    241       TNFR-CYS 4.
FT   REPEAT      243    281       TNFR-CYS 5.
FT   REPEAT      282    325       TNFR-CYS 6.
FT   DOMAIN      347    377       PRO/SER/THR-RICH.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    276    276       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   595 AA;  63747 MW;  7A407CC78A6E0BC8 CRC64;


  Query Match             9.8%;  Score 241;  DB 1;  Length 595;
  Best Local Similarity   22.0%;  Pred. No. 1.7e-07;
  Matches  113;  Conservative   41;  Mismatches  183;  Indels  176;  Gaps   17;

Qy      11 AVGLELWAAAHALPAQVAFTPYAPEPGSTC--RLREYYDQTAQMCCSKCSPGQHAKVFCT 68
           |:||    |  | |    |          ||      |||:  : || :|  |      |
Db       7 ALGLLFLGALRAFPQDRPFE-------DTCHGNPSHYYDKAVRRCCYRCPMGLFPTQQCP 59

Qy      69 KTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCAL 128
           :       ||   |    :    | :| :    | ||   |    :|:| |||| :|:
Db      60 QRPTDCRKQCEPDYYL---DEADRCTACVTCSRDDLVEKTPCAWNSSRVCECRPGMFCST 116

Qy     129 SKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPG---------------------- 167
           |    |  |      |  |  |  |||   : ||:| :||
Db     117 SAVNSCARCFFHSVCPAGMIVKFPGTAQKNTVCEPASPGVSPACASPENCKEPSSGTIPQ 176

Qy     168 ---------TFSNTT------------------------------------------- 173
                     | | :|
Db     177 AKPTPVSPATSSASTMPVRGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQPCPEG 236

Qy     174 ----------------------------------------SSTDICRPHQICNVVAIPG 192
                                                    | |  |||  ||   |
Db     237 SGDCRKQCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAWNSSRTCECRPGMICATSATNS 296

Qy     193 NASMDAVCTSTSPTRSMAPGAVHLPQ------------PVSTRSQHTQPTPE-----PST 235
                 |    |    |   |  ||            |: |:     ||||      ||
Db     297 -------CARCVPYPICAAETVTKPQDMAEKDTTFEAPPLGTQPD-CNPTPENGEAPAST 348

Qy     236 APSTSFL--------LPMGPSPP-AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQ 286
           :|: | |         ||:  | | |  |||    |  | ::    | |:::   :  ::
Db     349 SPTQSLLVDSQASKTLPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVVGSSAFLLCH 408

Qy     287 VKKKPLCLQREAKVPHL--PADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPT 344
              :  | :|  :  ||  |      |  |: : |: : |  ||: | | ||  :  |
Db     409 ---RRACRKRIRQKLHLCYPVQ----TSQPKLE-LVDSRPRRSSTQLRSGASVTEPVAEE 460

Qy     345 R---NQPQAPGVEASGAGEARASTGSSDSSPGG 374
           |   :||      : ||     |    |:|| |
Db     461 RGLMSQPLMETCHSVGAAYLE-SLPLQDASPAG 492


Search completed: August 21, 2002, 10:06:50
Job time: 763 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:47 ; Search time 31.43 Seconds
(without alignments)
2537.406 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2279	92.3	425	4	Q16042	Q16042 homo sapien
2	1498	60.7	482	11	O88734	O88734 mus musculu
3	1477	59.8	459	11	Q62327	Q62327 mus musculu
4	1375	55.7	433	11	Q91ZM6	Q91zm6 rattus norv
5	826	33.5	161	4	Q9UJQ3	Q9ujq3 homo sapien
6	503.5	20.4	175	11	Q9WUL4	Q9wul4 rattus norv
7	482	19.5	92	4	Q9UIG9	Q9uig9 homo sapien
8	409	16.6	78	4	Q9UIH0	Q9uih0 homo sapien
9	390.5	15.8	349	12	O57101	O57101 monkeypox v
10	389.5	15.8	349	12	O57291	O57291 monkeypox v
11	389.5	15.8	349	12	O57102	O57102 monkeypox v
12	389	15.8	348	12	O57277	O57277 monkeypox v
13	389	15.8	348	12	O57103	O57103 monkeypox v
14	389	15.8	348	12	O57108	O57108 monkeypox v
15	386.5	15.7	349	12	O57099	O57099 monkeypox v
16	385	15.6	349	12	O57284	O57284 camelpox vi
17	385	15.6	349	12	O57098	O57098 camelpox vi
18	383.5	15.5	349	12	O57100	O57100 monkeypox v
19	381.5	15.5	349	12	Q89098	Q89098 variola vir
20	381.5	15.5	349	12	O57111	O57111 variola vir
21	381	15.4	347	12	O57115	O57115 cowpox viru
22	381	15.4	349	12	O57097	O57097 camelpox vi
23	379.5	15.4	348	12	Q85407	Q85407 variola vir
24	379.5	15.4	348	12	O57112	O57112 variola vir
25	378	15.3	347	12	O57119	O57119 cowpox viru
26	377	15.3	360	12	O57118	O57118 cowpox viru
27	376.5	15.3	349	12	Q89118	Q89118 variola vir
28	376.5	15.3	349	12	O57110	O57110 variola vir
29	374	15.2	351	12	O57117	O57117 cowpox viru
30	374	15.2	351	12	O57121	O57121 cowpox viru
31	373	15.1	351	12	O73559	O73559 cowpox viru
32	373	15.1	355	12	Q85308	Q85308 unidentifie
33	371.5	15.1	349	12	O57109	O57109 variola vir
34	370.5	15.0	350	12	O57116	O57116 cowpox viru
35	368	14.9	349	12	O57305	O57305 cowpox viru
36	359	14.5	350	12	O57123	O57123 cowpox viru
37	354.5	14.4	326	12	O57122	O57122 cowpox viru
38	351.5	14.2	300	4	O95407	O95407 homo sapien
39	345.5	14.0	326	12	O57120	O57120 cowpox viru
40	343.5	13.9	655	4	O75509	O75509 homo sapien
41	339	13.7	316	12	O57092	O57092 ectromelia
42	339	13.7	320	12	O57300	O57300 ectromelia
43	339	13.7	320	12	O57091	O57091 ectromelia
44	330	13.4	320	12	O57079	O57079 cowpox viru
45	330	13.4	322	12	O72761	O72761 cowpox viru

ALIGNMENTS

RESULT 1
Q16042
ID Q16042 PRELIMINARY; PRT; 425 AA.
AC Q16042;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
DR EMBL; S63368; AAB19824.2; -.
DR HSSP; P25942; 1CDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;

Query Match 92.3%; Score 2279; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.2e-168;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSC 96
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      1 GSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSC 60

Qy     97 GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTET 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTET 120

Qy    157 SDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHL 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHL 180

Qy    217 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII 240

Qy    277 GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSAS 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSAS 300

Qy    337 ALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQ 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQ 360

Qy    397 CSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDA 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDA 420

Qy    457 GMKPS 461
          |||||
Db    421 GMKPS 425
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RESULT   2
O88734
ID   O88734      PRELIMINARY;      PRT;   482 AA.
AC   O88734;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P80 TNF-ALPHA RECEPTOR.
GN   TNFR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98414512; PubMed=9740674;
RA   Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT   "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT   and Characterization of the two Transcripts.";
RL   Genomics 52:79-98(1998).
DR   EMBL; Y14619; CAA74969.1; -.
DR   EMBL; Y14620; CAA74969.1; JOINED.
DR   EMBL; Y14621; CAA74969.1; JOINED.
DR   EMBL; Y14622; CAA74969.1; JOINED.
DR   EMBL; Y14623; CAA74969.1; JOINED.
DR   EMBL; Y14679; CAA74969.1; JOINED.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
SQ   SEQUENCE   482 AA;  51106 MW;  F6C15046B48FF83C CRC64;
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  Query Match             60.7%;  Score 1498;  DB 11;  Length 482;
  Best Local Similarity   62.8%;  Pred. No. 4e-108;
  Matches  297;  Conservative   49;  Mismatches  111;  Indels   16;  Gaps    9;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
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          ||| |:| ||   |:|||  | :||||  ||| ||||  |:: :||||: |||||:|| |
Db      1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy     60 GQHAKVFCTKTSDTVC-DS------CEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTR 112
          ||: | || ||||||| ||       || | |||:||    |||| | ||:|||||:|||:
Db     61 GQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTK 120

Qy    113 EQNRICTCRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSN 171
          :|||:| |  | ||||     | || |  | || ||||||        :|:|| |||||||:
Db    121 QQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSD 180

Qy    172 TTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTP 231
          ||||||:||||:||:::|||||||| ||||   ||| |  |  ::: ||  ||||     |
Db    181 TTSSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEP 240

Qy    232 EPSTAPSTSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKK 290
          ||  |  | |  :| :|  | || |  :||:||||||:||||::|:||| |: | |||
Db    241 GPSQTP--SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK 298

Qy    291 PLCLQREAKVPHLPADKARGTQGPEQQHLLITAP-SSSSSSLESSASALDRRAPTRNQPQ 349
          | ||||:|||||:| :|::   | |||||| ||| |||||||||||| |||||    ||
Db    299 PSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSSLESSASAGDRRAPPGGHPQ 358

Qy    350 APGV-EASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDT 408
          |  : || |: |||||:  |||| | ||| ||||||||||||||||||||:|:||
Db    359 ARVMAEAQGSQEARASSRISDSSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDP 418

Qy    409 DSSPSESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |: || ||||||||||:|||  :|  || |||   : |||||||||| |||||
Db    419 DAKPSASPKDEQVPFSQEECPSQSPYETTETL--QSHEKPLPLGVPDMGMKPS 469
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RESULT   3
Q62327
ID   Q62327      PRELIMINARY;      PRT;   459 AA.
AC   Q62327;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT   linked to autoimmune diabetes in NOD mice.";
RL   Genomics 0:0-0(0).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RX   MEDLINE=95178848; PubMed=7873884;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Allelic variation of the type 2 tumor necrosis factor receptor
RT   gene.";
RL   Mamm. Genome 5:726-727(1994).
DR   EMBL; X76401; CAA53981.1; -.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   VARIANT      87     87       S -> T.
FT   VARIANT      93     93       T -> I.
FT   VARIANT     268    268       F -> I.
FT   VARIANT     345    345       S -> F.
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FT   VARIANT     421    421       Y -> C.
SQ   SEQUENCE   459 AA;  48686 MW;  6C51D2CF1C4626DF CRC64;


  Query Match             59.8%;  Score 1477;  DB 11;  Length 459;
  Best Local Similarity   63.8%;  Pred. No. 1.6e-106;
  Matches  287;  Conservative   47;  Mismatches  108;  Indels    8;  Gaps    6;

Qy      16 LWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSPGQHAKVFCTKTSDTV 74
           |||  | :|||| |||| |||| |:: :|||| |||||:|| |||: | || ||||||
Db       1 LWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNKTSDTV 60

Qy      75 CDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEG- 133
           |  || | |||:||    |||| | ||:|||||:|||::|||:| |  | ||||    |
Db      61 CADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS 120

Qy     134 CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGN 193
           || |  | || ||||||       :|:|| |||||||:||||||:||||:||:::|||||
Db     121 CRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICSILAIPGN 180

Qy     194 ASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 253
           || ||||   ||| |  |  ::: ||  |||||     | ||  |  | |  :| :|  |
Db     181 ASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP--SILTSLGSTPIIEQ 238

Qy     254 ST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQ 312
           || |  :||:|||||||:||||::|:||| |: | |||| ||||:|||||:| :|::
Db     239 STKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVPDEKSQDAV 298

Qy     313 GPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EASGAGEARASTGSSDSS 371
           | |||||| |||||||||||||||| |||||    |||  : || |: |||||:  ||||
Db     299 GLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISDSS 358

Qy     372 PGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFR 431
           | ||| ||||||||||||||||||||||:|:|| |: || |||||||||:|||  :
Db     359 HGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASPKDEQVPFSQEECPSQ 418

Qy     432 SQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |  || |||   : |||||||||| |||||
Db     419 SPYETTETL--QSHEKPLPLGVPDMGMKPS 446


RESULT   4
Q91ZM6
ID   Q91ZM6      PRELIMINARY;      PRT;   433 AA.
AC   Q91ZM6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT   "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT   capillary endothelial cells and participate in TNF-alpha transport
RT   through the blood-brain barrier.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420214; AAL16021.1; -.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  45723 MW;  75736D835E72CA4A CRC64;


  Query Match             55.7%;  Score 1375;  DB 11;  Length 433;
  Best Local Similarity   61.3%;  Pred. No. 1.2e-98;
  Matches  268;  Conservative   48;  Mismatches  113;  Indels    8;  Gaps    6;

Qy      21 HALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCE 79
           | :|||:|  ||| |||| |:: :|||| |||||:|| |||:|| || |||||||  |
Db       1 HTVPAKVVLTPYKPEPGNQCQISQEYYDKKAQMCCAKCPPGQYAKHFCNKTSDTVCADCA 60

Qy      80 DSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEG-CRLCA 138
              :||:|| :  |||| | || |||||  ||::|||:| |    ||||    | || |
Db      61 AGMFTQVWNHLHTCLSCSSSCSDDQVETHNCTKKQNRVCACNADSYCALKLHSGNCRQCM 120

Qy     139 PLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198
           | || |||||||  |   :|:|  |||||||:||||||:||||:||:::|||||||  ||
Db     121 KLSKCGPGFGVARSRTSNGNVICSACAPGTFSDTTSSTDVCRPHRICSILAIPGNASTDA 180

Qy     199 VCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS-TGD 257
           || | ||| |  |  ::: ||  ||||     | ||  |     : :| :|  | | ||
Db     181 VCASESPTPSAVPRTIYVSQPEPTRSQPMDQEPGPSQTPHIP--VSLGSTPIIEPSITGG 238

Qy     258 FALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQ 317
           :||:|||||:| ||||::|: || |: | |||| |||||  ||||| :|::   | |||
Db     239 ISLPIGLIVGLTTLGLLMLGLANCFILVQRKKKPSCLQRETMVPHLPDEKSQDAVGLEQQ 298

Qy     318 HLLITAPSSSSSSLESSASALDRRAPTRNQPQA-PGVEASGAGEARASTGSSDSSPGGHG 376
           ||| ||||||||||||||| |||||    |||    || |: || | : |||| | ||
Db     299 HLLTTAPSSSSSSLESSASAGDRRAPPGVIPQARVTAEAQGSQEACAGSRSSDSSHGSHG 358

Qy     377 TQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECAFRSQLET 436
           | ||||||||||||||||||||:|:|| |::|| ||||||||||:|||  :|| ||
Db     359 THVNVTCIVNVCSSSDHSSQCSSQASTTVGDPDANPSGSPKDEQVPFSQEECPSQSQWET 418

Qy     437 PETLLGSTEEKPLPLGV 453
           |||     :|| ||||
Db     419 TETL--QNHDKPFPLGV 433


RESULT   5
Q9UJQ3
ID   Q9UJQ3      PRELIMINARY;      PRT;   161 AA.
AC   Q9UJQ3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   DJ1118D24.3 (TUMOR NECROSIS FACTOR RECEPTOR 2 (75 KDA) (TNF BINDING
DE   PROTEIN 2, TBPII, TNF-R2, CD120B, TNFBR)) (FRAGMENT).
GN   TNFR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Heath P.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL031276; CAA20343.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   161 AA;  16449 MW;  E6C96E774B5CF7B0 CRC64;


  Query Match             33.5%;  Score 826;  DB 4;  Length 161;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-56;
  Matches  161;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 60

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 120

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||||
Db     121 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 161


RESULT   6
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Q9WUL4
ID   Q9WUL4      PRELIMINARY;      PRT;   175 AA.
AC   Q9WUL4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE DAWLEY; TISSUE=OVARY;
RA   Balchak S.K., Marcinkiewicz J.L.;
RT   "Evidence for the Presence of Tumor Necrosis Factor Alpha Receptors
RT   During Ovarian Development in the Rat.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF142499; AAD30148.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00208; TNFR; 1.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     175    175
SQ   SEQUENCE   175 AA;  18201 MW;  499EEADAAB21ED8B CRC64;


  Query Match             20.4%;  Score 503.5;  DB 11;  Length 175;
  Best Local Similarity   55.9%;  Pred. No. 1.3e-31;
  Matches   99;  Conservative   23;  Mismatches   52;  Indels    3;  Gaps    2;

Qy     147 FGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTSTSPT 206
           ||||   |   :|:|  |||||||:||||||:||||:||:::|||||||| |||| | |||
Db       1 FGVASSRTSNGNVICSACAPGTFSDTTSSTDVCRPHRICSILAIPGNASTDAVCASESPT 60

Qy     207 RSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS-TGDFALPVGLI 265
           |  |  ::: ||  |||| | ||  |     : :| :|  | | ||  :||:|||
Db      61 PSAGPRTIYVSQPEPTRSQPMGQEPGPSQTPHIP--VSLGSTPIIEPSITGGISLPIGLI 118

Qy     266 VGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPEQQHLLIT 322
           ||:| ||||::|:  | |: | |||| ||||  ||||| ||::   | |||||| |
Db     119 VGLTTLGLLMLGLATCFILVQRKKKPSCLQRETMVPHLPDDKSQDAIGLEQQHLLTT 175


RESULT   7
Q9UIG9
ID   Q9UIG9      PRELIMINARY;      PRT;    92 AA.
AC   Q9UIG9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN   TNFR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21069356; PubMed=11197692;
RA   Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT   "New single nucleotide polymorphisms in the coding region of human
RT   TNFR2: association with systemic lupus erythematosus.";
RL   Genes Immun. 1:501-503(2000).
DR   EMBL; AB030952; BAA89055.1; -.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   92 AA;  9530 MW;  89BEDE40B7CC4FE1 CRC64;


  Query Match             19.5%;  Score 482;  DB 4;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-30;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     370 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 60

Qy     430 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||
Db      61 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 92


RESULT   8
Q9UIH0
ID   Q9UIH0      PRELIMINARY;      PRT;    78 AA.
AC   Q9UIH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 2 (FRAGMENT).
GN   TNFR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21069356; PubMed=11197692;
RA   Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT   "New single nucleotide polymorphisms in the coding region of human
RT   TNFR2: association with systemic lupus erythematosus.";
RL   Genes Immun. 1:501-503(2000).
DR   EMBL; AB030951; BAA89054.1; -.
KW   Receptor.
FT   NON_TER       1      1
FT   VARIANT      48     48       K -> E.
FT   NON_TER      78     78
SQ   SEQUENCE   78 AA;  7841 MW;  3A219A37EAFE0719 CRC64;


  Query Match             16.6%;  Score 409;  DB 4;  Length 78;
  Best Local Similarity   98.7%;  Pred. No. 1.1e-24;
  Matches   77;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLP 244
           |||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db       1 CNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPKPSTAPSTSFLLP 60

Qy     245 MGPSPPAEGSTGDFALPV 262
           ||||||||||||||||||
Db      61 MGPSPPAEGSTGDFALPV 78


RESULT   9
O57101
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1977 (77-0666);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; O14763; 1D0G.
```

```
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38311 MW;  02F65B00CFB858BE CRC64;


  Query Match             15.8%;  Score 390.5;  DB 12;  Length 349;
  Best Local Similarity   41.8%;  Pred. No. 1.5e-22;
  Matches   77;  Conservative   21;  Mismatches   71;  Indels   15;  Gaps    5;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN--------VVAIPGNASMDAVCTS 202
             | | ||:| || |||:|:| |||| | |    |         :   | |   |  ||
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINLYPVN---DTSCTR 196

Qy     203 TSPT 206
           |: |
Db     197 TTTT 200


RESULT  10
O57291
ID   O57291      PRELIMINARY;      PRT;   349 AA.
AC   O57291;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88144; AAB94369.1; -.
DR   EMBL; U87842; AAB94359.1; -.
DR   EMBL; U87994; AAB94365.1; -.
DR   EMBL; U87995; AAB94366.1; -.
DR   EMBL; U88143; AAB94368.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   349 AA;  38295 MW;  CBD2C949ED2B8E7C CRC64;


  Query Match             15.8%;  Score 389.5;  DB 12;  Length 349;
  Best Local Similarity   41.8%;  Pred. No. 1.8e-22;
  Matches   77;  Conservative   21;  Mismatches   71;  Indels   15;  Gaps    5;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN--------VVAIPGNASMDAVCTS 202
             | | ||:| || |||:|:| |||| | |    |         :   | |   |  ||
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINLYPVN---DTSCTR 196

Qy     203 TSPT 206
           |: |
Db     197 TTTT 200


RESULT  11
O57102
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BENIN-1978 (78-3945);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38308 MW;  CBD2C949F994C59C CRC64;


  Query Match             15.8%;  Score 389.5;  DB 12;  Length 349;
  Best Local Similarity   41.8%;  Pred. No. 1.8e-22;
  Matches   77;  Conservative   21;  Mismatches   71;  Indels   15;  Gaps    5;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGASGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN--------VVAIPGNASMDAVCTS 202
             | | ||:| || |||:|:| |||| | |    |         :   | |   |  ||
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINLYPVN---DTSCTR 196

Qy     203 TSPT 206
           |: |
Db     197 TTTT 200


RESULT  12
O57277
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
```

```
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  54019521556C2D8F CRC64;
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  Query Match             15.8%;  Score 389;  DB 12;  Length 348;
  Best Local Similarity   42.1%;  Pred. No. 2e-22;
  Matches   77;  Conservative   22;  Mismatches   70;  Indels   14;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:|||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRP--HQICNVVAI-----PGNASMDAVCTST 203
           | | ||:| || |||:|:| |||| | |      | : :     | |   |  || |
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVN---DTSCTRT 196

Qy     204 SPT 206
           : |
Db     197 TTT 199
```

```
RESULT  13
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979 (79-0005);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;
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  Query Match             15.8%;  Score 389;  DB 12;  Length 348;
  Best Local Similarity   42.1%;  Pred. No. 2e-22;
  Matches   77;  Conservative   22;  Mismatches   70;  Indels   14;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:|||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRP--HQICNVVAI-----PGNASMDAVCTST 203
           | | ||:| || |||:|:| |||| | |      | : :     | |   |  || |
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVN---DTSCTRT 196

Qy     204 SPT 206
           : |
Db     197 TTT 199
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RESULT  14
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970 (CONGO-8);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;
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  Query Match             15.8%;  Score 389;  DB 12;  Length 348;
  Best Local Similarity   42.1%;  Pred. No. 2e-22;
  Matches   77;  Conservative   22;  Mismatches   70;  Indels   14;  Gaps    6;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    |||| | ||:|| |    ||| |    ||  |:|||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRP--HQICNVVAI-----PGNASMDAVCTST 203
           | | ||:| || |||:|:| |||| | |      | : :     | |   |  || |
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVEINLYPVN---DTSCTRT 196

Qy     204 SPT 206
           : |
```

```
Db    197 TTT 199


RESULT  15
O57099
ID   O57099      PRELIMINARY;      PRT;   349 AA.
AC   O57099;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SIERRA LEONE-1970 (70-0266);
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87843; AAB94360.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38321 MW;  FE449028CC933F57 CRC64;


  Query Match             15.7%;  Score 386.5;  DB 12;  Length 349;
  Best Local Similarity   41.8%;  Pred. No. 3.1e-22;
  Matches   77;  Conservative   21;  Mismatches   71;  Indels   15;  Gaps    5;

Qy      31 PYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWV 90
           |:||  |  |:  ||  ::  :||  | || :|   |   ::| |  |   |:|   | :
Db      24 PHAPSNGK-CKDNEY--RSRNLCCLSCPPGTYASRLCDSKTNTQCTPCGSDTFTSHNNHL 80

Qy      91 PECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFGVA 150
             ||||  || |:||||::|    ||||  | ||:|| |    ||| |    ||  |:||:
Db      81 QACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGALGCRTCISKTKCGIGYGVS 140

Qy     151 RPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICN--------VVAIPGNASMDAVCTS 202
             | | ||:| || |||:|:| |||| | |    |        :   | |   |  ||
Db     141 -GYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDVEINLYPVN---DTSCTR 196

Qy     203 TSPT 206
           |: |
Db     197 TTTT 200


Search completed: August 21, 2002, 10:06:30
Job time: 763 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 434.34 Seconds
(without alignments)
117.892 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
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18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2468	100.0	461	12	AAR11141	Human TNF-R deduce
2	2468	100.0	461	14	AAR42058	Fibroblast derived
3	2468	100.0	461	21	AAB18717	A human tumour nec
4	2462	99.8	461	12	AAR11001	40kD TNF inhibitor
5	2462	99.8	461	21	AAB37801	Human tumour necro
6	2462	99.8	461	21	AAB01342	Death receptor. H
7	2462	99.8	461	22	AAB35331	Human TNF receptor
8	2462	99.8	461	22	AAB36698	Human tumour necro
9	2462	99.8	461	22	AAB37686	Human 40 kDa TNF i
10	2394	97.0	461	16	AAR72504	p75 Tumour Necrosi
11	2376	96.3	461	15	AAR51002	Sequence of human
12	2051.5	83.1	392	20	AAY30935	Human tumour necro
13	2051.5	83.1	392	22	AAB86818	Human TNFBP-associ
14	2050.5	83.1	392	12	AAR11605	Human 75kD TNF-bin
15	1506	61.0	474	12	AAR11142	TNF-R deduced from
16	1433	58.1	518	22	AAB70001	sTNFR(075):Fc fusi
17	1433	58.1	518	22	AAB50080	TNFR:Fc fusion pro
18	1424	57.7	518	15	AAR51003	Sequence of a reco
19	1404	56.9	485	13	AAR24016	Fusion protein TNF
20	1381	56.0	248	21	AAY94718	Human type 2 tumou
21	1318	53.4	235	21	AAY54443	Wild type N-termna
22	1315	53.3	235	21	AAY54440	Amino acid sequenc
23	1315	53.3	235	21	AAY54441	Amino acid sequenc
24	1312	53.2	235	19	AAW59665	Human soluble tumo
25	1312	53.2	235	19	AAW52270	Tumour necrosis fa
26	1312	53.2	235	20	AAW89234	Tumour necrosis in
27	1312	53.2	235	21	AAY54442	A K108R/K120R muta
28	1312	53.2	235	22	AAB37685	Human 40 kDa TNF i
29	1263	51.2	227	22	AAB66981	Tnfr2 protein. Un
30	1256	50.9	225	21	AAY77463	Primate protein se
31	1116	45.2	198	21	AAY94720	Human type 2 tumou
32	1028	41.7	183	16	AAR77421	BamTP delta53 nerv
33	937	38.0	165	21	AAB00014	Peptide fragment o
34	935	37.9	163	21	AAY94712	Tumour necrosis fa
35	856	34.7	159	22	AAB37683	Human 40 kDa TNF i
36	794.5	32.2	258	22	AAB50082	Rat TNFR (p80) ext
37	794.5	32.2	487	22	AAB50084	TNFR:Fc fusion pro
38	770	31.2	227	21	AAY77462	Rodent protein seq
39	707	28.6	122	19	AAW52271	Truncated soluble
40	695	28.2	120	22	AAB66991	Human TNF-II pepti
41	551	22.3	93	22	AAB37684	Human 40 kDa TNF i
42	477	19.3	802	16	AAR70111	TBPII-GBP 130 fusi
43	470	19.0	802	16	AAR70112	TNF-R-GBP 130 fusi
44	453	18.4	77	20	AAW94641	TNF-R extracellula
45	453	18.4	77	22	AAB69193	Human TNF-R extrac

ALIGNMENTS

RESULT 1
AAR11141
ID AAR11141 standard; Protein; 461 AA.
XX
AC AAR11141;
XX
DT 24-MAY-1991 (first entry)
XX
DE Human TNF-R deduced from clone 1.
XX
KW Tumour necrosis factor receptor; immune response; inflammation;
KW cachexia; septic shock.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= signal sequence
FT Protein 23..461
FT /label= TNF receptor
FT Domain 258..287
FT /label= transmembrane region
XX
PN EP418014-A.
XX
PD 20-MAR-1991.
XX
PF 10-SEP-1990; 90EP-0309875.
XX
PR 10-MAY-1990; 90US-0523635.
PR 11-SEP-1989; 89US-0405370.
PR 13-OCT-1989; 89US-0421417.
XX
PA (IMMU-) IMMUNEX CORP.

```
XX
PI   Smith CA,  Goodwin RG,  Beckmann PM;
XX
DR   WPI; 1991-082230/12.
DR   N-PSDB; AAQ10990.
XX
PT   New tumour necrosis factor -alpha and -beta receptors - and DNA
PT   encoding these used to regulate immune responses in treatment of
PT   cachexia, septic shock or side-effects of cytokine therapy.
XX
PS   Disclosure; Fig 2; 41pp; English.
XX
CC   The sequence was deduced from a DNA sequence obtd. from a clone
CC   isolated from a library prepd. from a human fibroblast cell line,
CC   WI-26 VA4 (ATCC CCL 95.1).  The clone is deposited as Accession No.
CC   68088 under the name pCAV/NOT-TNF-R. The DNA can be truncatd to
CC   produce sequences which express soluble receptor comprising
CC   residues 1-235, 1-185 or 1-163 of the protein.
CC   See also AAR11142.
XX
SQ   Sequence   461 AA;


  Query Match             100.0%;  Score 2468;  DB 12;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-152;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   2
AAR42058
ID   AAR42058 standard; Protein; 461 AA.
XX
AC   AAR42058;
XX
DT   29-APR-1994  (first entry)
XX
DE   Fibroblast derived TNF-R.
XX
KW   Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW   IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW   rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW   pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW   graft verses host disease; sepsis; inflammation; allergy;
KW   autoimmune dysfunction.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /note= "Signal peptide"
FT   Protein         23..461
FT                   /note= "Mature hTNF-R"
FT   Peptide         23..185
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         23..207
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         23..257
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         23..206
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         23..204
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         1..206
FT                   /note= "Preferred soluble TNF-R"
FT   Peptide         1..204
FT                   /note= "Preferred soluble TNF-R"
XX
PN   WO9319777-A.
XX
PD   14-OCT-1993.
XX
PF   26-MAR-1993;   93WO-US02938.
XX
PR   30-MAR-1992;   92US-0860710.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Smith CA;
XX
DR   WPI; 1993-336592/42.
DR   N-PSDB; AAQ49931.
XX
PT   New fusion protein tumour necrosis factor and human interleukin-1
PT   receptor - useful in therapy, diagnosis and assays of e.g.
PT   rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
PS   Claim 5; Fig 2; 85pp; English.
XX
CC   The sequences given in AAR42058-59 repressent human tumour necrosis
CC   factor receptor (TNF-R) and the sequences in AAR42060-61 represent
CC   human interleukin-1 receptor (IL-1R).  These sequences were used in
CC   the production of a fusion protein which conformed to one of the
CC   formulae:
CC        TNF-R-linker-TNF-R-linker-IL-1R
CC        IL-1R-linker-TNF-R-linker-TNF-R or
CC        TNF-R-linker-TNF-R
CC   The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC   Ser, Thr and Ala.  These linkers separate the individual moeities
CC   by such a distance that each component of the fusion protien is
CC   capable of folding into the secondary or tertiary structure required
CC   for its biological activity.  These fusion proteins may be used in
CC   therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC   particularly in conditions in which both TNF and IL-1 play a causitive
CC   role.  They may be used to treat cachexia, rheumatoid arthritis,
CC   diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC   cerebral malaria, allograft and xenograft rejection in graft verses
CC   host disease, sepsis, septic shock, inflammation, allergies and
CC   autoimmune dysfunctions.
XX
SQ   Sequence   461 AA;


  Query Match             100.0%;  Score 2468;  DB 14;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-152;
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  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapssssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   3
AAB18717
ID   AAB18717 standard; Protein; 461 AA.
XX
AC   AAB18717;
XX
DT   22-JAN-2001  (first entry)
XX
DE   A human tumour necrosis factor family receptor (TNF-RII).
XX
KW   Human; tumour necrosis factor family receptor; TR1; tumour growth;
KW   cell proliferation; chlamydia infection; immunodeficiency; septic shock;
KW   T-cell mediated autoimmune disease; acquired immunodeficiency syndrome;
KW   AIDS; cerebral malaria; graft rejection; cytotoxicity; cachexia;
KW   apoptosis; inflammation; cancer; cardiovascular disease; angiogenesis;
KW   inflammatory disease; atherosclerosis; diabetes mellitus; allergy;
KW   neurological disorder; autoimmune disease; wound healing; bone formation;
KW   osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO200054651-A2.
XX
PD   21-SEP-2000.
XX
PF   15-MAR-2000; 2000WO-US06592.
XX
PR   15-MAR-1999;   99US-0124489.
PR   26-MAY-1999;   99US-0136248.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Greene JM,  Fleischmann RD,  Ni J;
XX
DR   WPI; 2000-618858/59.
XX
PT   Novel tumour necrosis factor family receptor for diagnosing and treating
PT   acquired immunodeficiency syndrome, cancer, cardiovascular diseases,
PT   inflammatory diseases and autoimmune diseases -
XX
PS   Claim 16; Page 24-25; 228pp; English.
XX
CC   The present sequence encodes human tumour necrosis factor family
CC   receptor (TNF-RII) polypeptide. The specification describes a TNF
CC   receptor designated TR1. An agonist to the TR1 receptor is useful for
CC   inhibiting tumour growth, to stimulate human cellular proliferation, to
CC   regulate immune response and antiviral response, to protect against the
CC   effects of ionising radiations, to protect against chlamydia infections,
CC   to regulate growth, and to treat immunodeficiencies such as in human
CC   immunodeficiency virus (HIV). An antagonist to the TR1 receptor is
CC   useful for treating T-cell mediated autoimmune diseases, acquired
CC   immunodeficiency syndrome (AIDS), septic shock, cerebral malaria, graft
CC   rejection, cytotoxicity, cachexia, apoptosis, and inflammation. TR1
CC   polynucleotides and polypeptides, and TR1 agonists and antagonists
CC   are useful for treating cancers, cardiovascular diseases, inflammatory
CC   diseases, atherosclerosis, diabetes mellitus, neurological disorders,
CC   autoimmune diseases, for promoting angiogenesis, for treating allergy,
CC   for wound healing, for regulating bone formation and for treating
CC   osteoporosis.
XX
SQ   Sequence   461 AA;


  Query Match             100.0%;  Score 2468;  DB 21;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-152;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapssssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   4
AAR11001
ID   AAR11001 standard; Protein; 461 AA.
XX
AC   AAR11001;
XX
DT   13-MAY-1991  (first entry)
XX
DE   40kD TNF inhibitor precursor.
XX
KW   Tumour necrosis factor; inhibitor.
```

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XX
OS   Homo sapiens.
XX
PN   AU9058976-A.
XX
PD   24-JAN-1991.
XX
PF   16-JUL-1990;   90AU-0058976.
XX
PR   07-FEB-1990;   90US-0479661.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
XX
PA   (SYNE-) SYNERGEN INC.
XX
DR   WPI; 1991-073847/11.
DR   N-PSDB; AAQ10907.
XX
PT   Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT   and -beta, useful as therapeutic agent.
XX
PS   Disclosure; Fig 39; 142pp; English.
XX
CC   The sequence comprises the entire 40 kD TNF inhibitor. The clone
CC   from which the sequence was deduced was isolated from a cDNA
CC   library prepd. from RNA form U937 cells treated with PMA/PHA.
CC   The whole gene can be inserted into expression vectors for prepn.
CC   of TNF inhibitor for use in the treatment of inflammatory and
CC   degenerative diseases.
CC   See also AAR10986 and AAR10984.
XX
SQ   Sequence   461 AA;


  Query Match             99.8%;  Score 2462;  DB 12;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   5
AAB37801
```

```
ID   AAB37801 standard; Protein; 461 AA.
XX
AC   AAB37801;
XX
DT   23-FEB-2001  (first entry)
XX
DE   Human tumour necrosis factor p75 receptor.
XX
KW   Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW   p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW   immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW   neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW   multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW   chronic myelogenous leukaemia; inflammatory bowel disease.
XX
OS   Homo sapiens.
XX
PN   WO200064479-A1.
XX
PD   02-NOV-2000.
XX
PF   26-APR-2000; 2000WO-US11700.
XX
PR   27-APR-1999;   99US-0301274.
XX
PA   (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI   Fredeking TM,  Ignatyev GM;
XX
DR   WPI; 2000-679646/66.
XX
PT   Novel compositions comprising tetracycline or tetracycline-like
PT   compounds for the treatment and/or prevention of acute inflammatory
PT   responses and diseases, e.g. septic shock and immune complex-induced
PT   colitis -
XX
PS   Disclosure; Page 169-171; 183pp; English.
XX
CC   The present sequence is given in a specification relating to novel
CC   compositions and methods containing tetracycline or tetracycline-like
CC   compounds for treating and/or preventing acute inflammatory responses and
CC   diseases. Such diseases include acute inflammatory conditions associated
CC   with viral haemorrhagic diseases (including diseases caused by
CC   Bunyaviridea, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC   parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC   disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC   transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC   immune complex-induced colitis, cerebrospinal fluid inflammation,
CC   multiple sclerosis, inflammatory responses associated with trauma,
CC   systemic inflammatory response syndrome (SIRS), adult respiratory
CC   distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC   and Crohn's disease.
XX
SQ   Sequence   461 AA;


  Query Match             99.8%;  Score 2462;  DB 21;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
```

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          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 phlpadkargtqgpeqqhllitapssssssslessasaldrraptrnqpqapgveasgage 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||
Db    421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   6
AAB01342
ID   AAB01342 standard; Protein; 461 AA.
XX
AC   AAB01342;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Death receptor.
XX
KW   UL144; death receptor; apoptosis; programmed cell death; FAS;
KW   TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW   human.
XX
OS   Homo sapiens.
XX
PN   WO200034335-A2.
XX
PD   15-JUN-2000.
XX
PF   03-DEC-1999;   99WO-US26035.
XX
PR   04-DEC-1998;   98US-0205018.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Leong C,  Phillips JH;
XX
DR   WPI; 2000-423383/36.
XX
PT   Purified or recombinant polypeptide for modulating apoptosis comprises
PT   a sequence which binds to an antibody specific for UL144 or its
PT   fragments
XX
PS   Disclosure; Page 74-75; 76pp; English.
XX
CC   A pure or recombinant polypeptide which binds to a polyclonal antibody
CC   specific for the mature UL144 is useful for screening molecules which
CC   block induction of apoptosis or interfere with antiapoptotic activity.
CC   The polypeptide is also useful for modulating apoptosis and useful in
CC   treatment of conditions associated with abnormal physiology or
CC   development, such as cancer or degenerative conditions and for
CC   regulation of viral infection and replication. At least five
CC   different death receptors are known, which include the CD95
CC   (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated
CC   protein (TRAMP), death receptor-6 (DR-6), and TNF-related
CC   apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
XX
SQ   Sequence   461 AA;

  Query Match             99.8%;  Score 2462;  DB 21;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 phlpadkargtqgpeqqhllitapssssssslessasaldrraptrnqpqapgveasgage 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||
Db    421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   7
AAB35331
ID   AAB35331 standard; Protein; 461 AA.
XX
AC   AAB35331;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TNF receptor SEQ ID NO: 6.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;   99US-0144087.
PR   18-AUG-1999;   99US-0149450.
PR   20-AUG-1999;   99US-0149712.
PR   10-SEP-1999;   99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Young PE;
XX
DR   WPI; 2001-112682/12.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
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```
PS   Disclosure; Page 377-378; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   461 AA;


  Query Match             99.8%;  Score 2462;  DB 22;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   8
AAB36698
ID   AAB36698 standard; Protein; 461 AA.
XX
AC   AAB36698;
XX
DT   15-MAR-2001  (first entry)
XX
DE   Human tumour necrosis factor receptor TNFR2 protein SEQ ID NO:3.
XX
KW   Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic;
KW   TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW   tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW   immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW   anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW   gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW   apoptotic cell death related disease; autoimmune disorder;
KW   cardiovascular disorder; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200071150-A1.
XX
PD   30-NOV-2000.
XX
PF   18-MAY-2000; 2000WO-US13515.
XX
PR   20-MAY-1999;   99US-0135164.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Wei Y,  Ruben SM,  Gentz RL,  Ni J;
XX
DR   WPI; 2001-041051/05.
XX
PT   Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT   necrosis factor receptor 5, useful in the diagnosis, treatment or
PT   prevention of cancer, autoimmune disorders and viral infection -
XX
PS   Disclosure; Fig 2; 285pp; English.
XX
CC   The present invention describes the human TRID protein (tumour necrosis
CC   factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC   intracellular domain, also referred to as tumour necrosis factor
CC   receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC   nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC   antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC   activities, and can be used in gene therapy. The TRID polynucleotides
CC   are useful for detecting complementary polynucleotides. TRID proteins and
CC   polynucleotides are useful in the treatment of tumours, resistance to
CC   parasite, bacteria and viruses, restenosis and graft versus host disease.
CC   They are also useful for inducing proliferation of T-cells, endothelial
CC   cells and certain haematopoietic cells, to regulate antiviral responses
CC   and to prevent certain autoimmune diseases after stimulation of TRID by
CC   an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC   polypeptides are useful for treating and/or preventing diseases
CC   associated with increased or decreased apoptotic cell death. The TRID
CC   polynucleotides, proteins, antibodies, agonists and antagonists are
CC   useful in the diagnosis, treatment or prevention of: (a) cancer;
CC   (b) autoimmune disorders; (c) diseases associated with increased
CC   apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC   present sequence represents a tumour necrosis factor receptor used in
CC   comparison with TRID in the exemplification of the present invention.
XX
SQ   Sequence   461 AA;


  Query Match             99.8%;  Score 2462;  DB 22;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||||
Db    421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT   9
AAB37686
ID   AAB37686 standard; Protein; 461 AA.
XX
AC   AAB37686;
XX
DT   02-MAR-2001  (first entry)
XX
DE   Human 40 kDa TNF inhibitor precursor.
XX
KW   TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; lymphotoxin.
XX
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995;   95US-0375242.
XX
PR   19-JUL-1990;   90US-0555274.
PR   09-JUL-1993;   93US-0090366.
PR   18-JUL-1989;   89US-0381080.
PR   11-DEC-1989;   89US-0450329.
PR   07-FEB-1990;   90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C,  King MW,  Hale KK,  Brewer MT,  Thompson RC;
PI   Vanderslice RW,  Vannice J,  Kohno T;
XX
DR   WPI; 2001-006443/01.
DR   N-PSDB; AAC83951.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross-linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PT   TNF  -
XX
PS   Example 12; Fig 39; 82pp; English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the precursor for 40 kDa TNF inhibitor. The 40 kDa
CC   TNF inhibitor can inhibit both TNF alpha and beta (lymphotoxin).
XX
SQ   Sequence   461 AA;


  Query Match             99.8%;  Score 2462;  DB 22;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 4.3e-152;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 qhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    181 phqicnvvaipgnasrdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 fllpmgpsppaegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 phlpadkargtqgpeqqhllitapssssssslessasaldrraptrnqpqapgveasgage 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||||
Db    421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT  10
AAR72504
ID   AAR72504 standard; Protein; 461 AA.
XX
AC   AAR72504;
XX
DT   31-OCT-1995  (first entry)
XX
DE   p75 Tumour Necrosis Factor Receptor.
XX
KW   Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
KW   receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          27..214
FT                   /label= TBPII.
FT   Domain          258..285
FT                   /label= Transmembrane domain.
FT   Misc-difference 259
FT                   /note= "Unidentified amino acid."
XX
PN   EP648783-A.
XX
PD   19-APR-1995.
XX
PF   11-OCT-1994;   94EP-0116015.
XX
PR   12-OCT-1993;   93IL-0107267.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (WALL/) WALLACH D.
XX
PI   Beletsky I,  Bigda J,  Mett I,  Wallach D;
XX
DR   WPI; 1995-148673/20.
DR   N-PSDB; AAQ89544.
XX
PT   Tumour necrosis factor (TNF) receptor ligand - used to increase
PT   inhibitory effect of a soluble TNF receptor
XX
PS   Disclosure; Figure 2; 18pp; English.
XX
CC   A ligand to a member of the tumour necrosis factor (TNF)/nerve
CC   growth factor (NGF) receptor family which binds either to the region
CC   of the 4th-Cys rich domain of the receptor, or to the region between
CC   it and the cell membrane may be used in the production of a
CC   pharmaceutical composition for increasing the inhibitory effect of a
```

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CC   soluble receptor of the TNF/NGF receptor family.  This sequence
CC   is the sequence of the p75 TNF receptor.
XX
SQ   Sequence   461 AA;


  Query Match             97.0%;  Score 2394;  DB 16;  Length 461;
  Best Local Similarity   96.4%;  Pred. No. 1.1e-147;
  Matches  451;  Conservative    0;  Mismatches    3;  Indels   14;  Gaps    2;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyapepgstcrlreyydqtaqmccskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qhakafctktsdtvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 rpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 phqicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfxlpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||       ||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpq-------gage 353

Qy     361 ARASTGSSDSSPGGHGTQ-------VNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPS 413
           ||||||||||||||||||       ||||| ||||||||||||||||||||||||||||
Db     354 arastgssdsspgghgtqapgveasvnvtctvnvcsssdhssqcssqasstmgdtdssps 413

Qy     414 ESPKDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     414 espkdeqvpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT  11
AAR51002
ID   AAR51002 standard; Protein; 461 AA.
XX
AC   AAR51002;
XX
DT   07-OCT-1994  (first entry)
XX
DE   Sequence of human tumour necrosis factor receptor type I
DE   (TNFRI).
XX
KW   Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= signal
FT   Peptide         22..461
FT                   /label= mature
XX
PN   WO9406476-A.
XX
PD   31-MAR-1994.
XX
PF   14-SEP-1993;   93WO-US08666.
XX
PR   15-SEP-1992;   92US-0946236.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Jacobs CA,  Smith CA;
XX
DR   WPI; 1994-118172/14.
DR   N-PSDB; AAQ45224.
XX
PT   Treating TNF mediated inflammatory diseases with TNF antagonist -
PT   esp. soluble form of TNF receptor, opt. as fusion protein with
PT   human immunoglobulin Fc region, esp. for treating arthritis
XX
PS   Disclosure; Page 28-30; 47pp; English.
XX
CC   AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
CC   cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
CC   having a mol. wt. of about 75-80 kDa.The cloning of the cDNA for
CC   TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
CC   is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
CC   preferred TNFRs of the present invention are soluble forms of TNFRI
CC   and TNFRII having at least 20 AAs. Soluble TNFR constructs are
CC   devoid of a transmembrane region but retain the ability to bind TNF.
CC   Examples of soluble TNFRs are huTNFRIdelta235, huTNFRIdelta185 and
CC   huTNFRIdelta163 which encode respectively AAs 1-235,1-185 and 1-163
CC   of AAR51002. An equivalent soluble TNFR is huTNFRIdeltax wherein x
CC   is selected from any one of AAs 163-235 of AAR51002.
XX
SQ   Sequence   461 AA;


  Query Match             96.3%;  Score 2376;  DB 15;  Length 461;
  Best Local Similarity   96.7%;  Pred. No. 1.6e-146;
  Matches  446;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           |||||||||||||||||||||||||||||| |||||||||||||:|| ||||||
Db       1 mapvavwaalavglelwaaahalpaqvaftpyarepgstcrlreyydqtaemcwskcspg 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           | |||||||||:||||||:||||:||||||||||||||||||||||||||| |||||
Db      61 qdakvfctktsdsvcdsceestytqvwnwvpeclscgsrcssdqvetqactreqkrictc 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||| || ||||||||||||||||||||||||||||||||| ||||||||| ||||||
Db     121 rpgwywalrkqegcrlcaplrkcrpgfgvarpgtetsdvvckpcgpgtfsnttswtdicr 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 rheicnvvaipgnasmdavctstsptrsmapgavhlpqpvstrsqhtqptpepstapsts 240

Qy     241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     241 fllpmgpsppaegstgdfglpvglivgvtalglliigvvncvimtqvkkkplclqreakv 300

Qy     301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 phlpadkargtqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgage 360

Qy     361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 arastgssdsspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeq 420

Qy     421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           |||||||||||||||||||||||||||||||||||||||||
Db     421 vpfskeecafrsqletpetllgsteekplplgvpdagmkps 461


RESULT  12
AAY30935
ID   AAY30935 standard; Protein; 392 AA.
XX
AC   AAY30935;
XX
DT   18-OCT-1999  (first entry)
XX
```

```
DE   Human tumour necrosis factor binding protein fragment.
XX
KW   Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KW   anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW   autoimmune glomerulonephritis; cerebral malaria; immune response;
KW   antagonist; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1..392
FT                   /note= "Partial sequence, no start codon given"
XX
PN   EP939121-A2.
XX
PD   01-SEP-1999.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 1999-480840/41.
DR   N-PSDB; AAZ09171.
XX
PT   New insoluble proteins, and fragments, that bind to tumor necrosis
PT   factor, used to treat e.g. septic shock or cerebral malaria
XX
PS   Claim 4a; Fig 4; 25pp; German.
XX
CC   This invention describes novel homogeneous insoluble proteins (I),
CC   their (in)soluble fragments (Ia) and their salts that can bind tumour
CC   necrosis factor (TNF). The products of the invention have
CC   anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC   to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC   glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC   (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC   diagnostic determination of TNF in body fluids. Antibodies raised against
CC   (I) are used for affinity purification of (I). This sequence represents
CC   a tumour necrosis factor binding protein fragment described in the method
CC   of the invention.
XX
SQ   Sequence   392 AA;

  Query Match             83.1%;  Score 2051.5;  DB 20;  Length 392;
  Best Local Similarity   98.7%;  Pred. No. 1.6e-125;
  Matches  387;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      71 SDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
           ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 sdsvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictcrpgwycalsk 60

Qy     131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI 190
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 qegcrlcaplpkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicrphqicnvvai 120

Qy     191 PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 250
           ||||| ||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db     121 pgnasrdavctstsptrsmapgavhlpqpvstrsqhtqpspepstapstsfllpmgpspp 180

Qy     251 AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARG 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 aegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakvphlpadkarg 240

Qy     311 TQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSS-D 369
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |

Db     241 tqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgagearastgssad 300

Qy     370 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 429
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 sspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeqvpfskeeca 360

Qy     430 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           ||||||||||||||||||||||||||||||||
Db     361 frsqletpetllgsteekplplgvpdagmkps 392


RESULT  13
AAB86818
ID   AAB86818 standard; Protein; 392 AA.
XX
AC   AAB86818;
XX
DT   12-NOV-2001  (first entry)
XX
DE   Human TNFBP-associated protein #2.
XX
KW   TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW   insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW   antiprotozoal; treatment; meningococcal sepsis; cerebral malaria;
KW   autoimmune glomerulonephritis.
XX
OS   Homo sapiens.
XX
PN   EP1132471-A2.
XX
PD   12-SEP-2001.
XX
PF   31-AUG-1990; 2001EP-0108117.
XX
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
PR   20-APR-1990;   90CH-0001347.
PR   31-AUG-1990;   90EP-0116707.
PR   31-AUG-1990;   99EP-0100703.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Loetscher H;
PI   Schlaeger E;
XX
DR   WPI; 2001-559312/63.
DR   N-PSDB; AAH48860.
XX
PT   New homogeneous, insoluble proteins that bind tumor necrosis factor
PT   (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
XX
PS   Claim 4a; Fig 4; 26pp; German.
XX
CC   This invention describes novel insoluble proteins (I), also their
CC   (in)soluble fragments and pharmaceutically acceptable salts, able to bind
CC   tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC   invention have antiinflammatory, immunosuppressive, antibacterial,
CC   antiprotozoal activity. (I), and related recombinant proteins, are used
CC   to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC   sepsis; development of autoimmune glomerulonephritis and cerebral
CC   malaria. Also (I), or antibodies specific for them, are used for
CC   diagnostic determination of TNF in body fluids, for affinity purification
CC   of TNF and for identifying (ant)agonists of TNF. This sequence represents
CC   a human TNF binding protein described in the method of the invention.
XX
SQ   Sequence   392 AA;

  Query Match             83.1%;  Score 2051.5;  DB 22;  Length 392;
  Best Local Similarity   98.7%;  Pred. No. 1.6e-125;
  Matches  387;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      71 SDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
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          ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 sdsvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictcrpgwycalsk 60

Qy    131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI 190
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 qegcrlcaplpkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicrphqicnvvai 120

Qy    191 PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 250
          ||||| ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db    121 pgnasrdavctstsptrsmapgavhlpqpvstrsqhtqpspepstapstsfllpmgpspp 180

Qy    251 AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARG 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 aegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakvphlpadkarg 240

Qy    311 TQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSS-D 369
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    241 tqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgagearastgssad 300

Qy    370 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeqvpfskeeca 360

Qy    430 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||
Db    361 frsqletpetllgsteekplplgvpdagmkps 392


RESULT  14
AAR11605
ID   AAR11605 standard; Protein; 392 AA.
XX
AC   AAR11605;
XX
DT   24-MAY-1991  (first entry)
XX
DE   Human 75kD TNF-binding protein.
XX
KW   Tumour Necrosis Factor; binding proteins; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /label= Ser, Thr
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990;   90EP-0116707.
XX
PR   20-APR-1990;   90CH-0001347.
PR   12-SEP-1989;   89CH-0003319.
PR   08-MAR-1990;   90CH-0000746.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Brockhaus M,  Dembic Z,  Gentz R,  Lesslauer W,  Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991-081851/12.
DR   N-PSDB; AAQ10956.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 1; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as aprobe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identifed and sequenced. Repeated sequencing showed a discrepancy
CC   at position 7 such that the third codon encodes either Thr or Ser.
CC   See also AAQ10955.
XX
SQ   Sequence   392 AA;


  Query Match             83.1%;  Score 2050.5;  DB 12;  Length 392;
  Best Local Similarity   98.7%;  Pred. No. 1.9e-125;
  Matches  387;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     71 SDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSK 130
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 sdxvcdscedstytqlwnwvpeclscgsrcssdqvetqactreqnrictcrpgwycalsk 60

Qy    131 QEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAI 190
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 qegcrlcaplpkcrpgfgvarpgtetsdvvckpcapgtfsnttsstdicrphqicnvvai 120

Qy    191 PGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 250
          ||||| ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db    121 pgnasrdavctstsptrsmapgavhlpqpvstrsqhtqpspepstapstsfllpmgpspp 180

Qy    251 AEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKVPHLPADKARG 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 aegstgdfalpvglivgvtalglliigvvncvimtqvkkkplclqreakvphlpadkarg 240

Qy    311 TQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGEARASTGSS-D 369
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    241 tqgpeqqhllitapsssssslessasaldrraptrnqpqapgveasgagearastgssad 300

Qy    370 SSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEECA 429
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 sspgghgtqvnvtcivnvcsssdhssqcssqasstmgdtdsspsespkdeqvpfskeeca 360

Qy    430 FRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||
Db    361 frsqletpetllgsteekplplgvpdagmkps 392


RESULT  15
AAR11142
ID   AAR11142 standard; Protein; 474 AA.
XX
AC   AAR11142;
XX
DT   24-MAY-1991  (first entry)
XX
DE   TNF-R deduced from mTNF-R clone 11.
XX
KW   Tumour necrosis factor receptor; immune response; inflammation;
KW   cachexia; septic shock.
XX
OS   Mus musculus strain C57BL/6.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= signal sequence
FT   Domain          234..265
FT                   /label= transmembrane region
XX
PN   EP418014-A.
XX
PD   20-MAR-1991.
XX
PF   10-SEP-1990;   90EP-0309875.
XX
PR   10-MAY-1990;   90US-0523635.
PR   11-SEP-1989;   89US-0405370.
PR   13-OCT-1989;   89US-0421417.
XX
PA   (IMMU-) IMMUNEX CORP.
```

XX
PI Smith CA, Goodwin RG, Beckmann PM;
XX
DR WPI; 1991-082230/12.
DR N-PSDB; AAQ10991.
XX
PT New tumour necrosis factor -alpha and -beta receptors - and DNA
PT encoding these used to regulate immune responses in treatment of
PT cachexia, septic shock or side-effects of cytokine therapy.
XX
PS Disclosure; Fig 3; 41pp; English.
XX
CC The sequence was deduced from a clone isolated from library prepd.
CC from a murine T helper cell line, 7B9.
CC See also AAR11141.
XX
SQ Sequence 474 AA;

Query Match 61.0%; Score 1506; DB 12; Length 474;
Best Local Similarity 62.8%; Pred. No. 5.3e-90;
Matches 292; Conservative 50; Mismatches 115; Indels 8; Gaps 6;

```
Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
           ||| |:| ||   |:||| | :|||| ||| |||| |:: :|||: |||||:|| |
Db       1 mapaalwvalvfelqlwatghtvpaqvvltpykpepgyecqisqeyydrkaqmccakcpp 60

Qy      60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
           ||: | || ||||||| || | |||:||    |||| | |::|||| :|||::|||:|
Db      61 gqyvkhfcnktsdtvcadceasmytqvwnqfrtclscsssscttdqveiractkqqnrvca 120

Qy     120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
           |  | || |   | || |  | || |||||       :|:|| |||||||:||||||:
Db     121 ceagrycdlkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtfsdttsstdv 180

Qy     179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
           ||||:||:::|||||| ||||   ||| |  |  ::: ||  ||||     | ||  |
Db     181 crphricsilaipgnastdavcapesptlsaiprtlyvsqpeptrsqpldqepgpsqtp- 239

Qy     239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
            | |  :| :|  | || |  :||:|||||||:||||::|:|||:|: | |||| ||||:
Db     240 -siltslgstpiieqstkggislpiglivgvtslgllmlglvnciilvqrkkkpsclqrd 298

Qy     298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
           |||||:| :|::   | |||||| |||||||||||||||| |||||    |||  : ||
Db     299 akvphvpdeksqdavgleqqhllttapsssssslessasagdrrappgghpqarvmaeaq 358

Qy     357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
           |  |||||:  |||| | ||| ||||||||||||||||||||||:|:|| |: || ||
Db     359 gfqearassrisdsshgshgthvnvtcivnvcsssdhssqcssqasatvgdpdakpsasp 418

Qy     417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
           ||||||||:|||  :|  || |||   : |||||||||| |||||
Db     419 kdeqvpfsqeecpsqspcettetl--qshekplplgvpdmgmkps 461
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Job time: 494 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 09:53:12 ; Search time 16.32 Seconds
(without alignments)
689.963 Million cell updates/sec

Title: US-09-800-909-2
Perfect score: 2468
Sequence: 1 MAPVAVWAALAVGLELWAAA.....GSTEEKPLPLGVPDAGMKPS 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2468	100.0	461	1	US-08-385-229-2	Sequence 2, Appli
2	2468	100.0	461	2	US-08-650-000-2	Sequence 2, Appli
3	2468	100.0	461	4	US-08-477-347-3	Sequence 3, Appli
4	2468	100.0	461	4	US-08-476-862-2	Sequence 2, Appli
5	2468	100.0	461	6	5395760-2	Patent No. 5395760
6	2462	99.8	461	4	US-09-042-785A-7	Sequence 7, Appli
7	2462	99.8	461	4	US-09-006-353A-4	Sequence 4, Appli
8	1512	61.3	474	2	US-08-650-000-4	Sequence 4, Appli
9	1512	61.3	474	4	US-09-042-785A-8	Sequence 8, Appli
10	1512	61.3	474	6	5395760-4	Patent No. 5395760
11	1433	58.1	518	1	US-08-385-229-4	Sequence 4, Appli
12	1404	56.9	486	1	US-08-243-010-1	Sequence 1, Appli
13	1312	53.2	235	4	US-09-326-394-4	Sequence 4, Appli
14	1263	51.2	227	3	US-08-974-022-48	Sequence 48, Appl
15	1263	51.2	227	4	US-08-795-445A-48	Sequence 48, Appl
16	1263	51.2	227	4	US-08-795-447A-48	Sequence 48, Appl
17	1263	51.2	227	4	US-08-974-186-48	Sequence 48, Appl
18	1263	51.2	227	4	US-08-795-446B-48	Sequence 48, Appl
19	931	37.7	163	2	US-08-219-237B-5	Sequence 5, Appli
20	931	37.7	163	4	US-08-477-347-13	Sequence 13, Appl
21	931	37.7	163	4	US-08-476-862-4	Sequence 4, Appli
22	931	37.7	163	4	US-08-468-560C-5	Sequence 5, Appli
23	924.5	37.5	164	2	US-08-232-087A-9	Sequence 9, Appli
24	695	28.2	120	3	US-08-974-022-42	Sequence 42, Appl
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26	695	28.2	120	4	US-08-795-447A-42	Sequence 42, Appl
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29	453	18.4	77	4	US-08-866-545-2	Sequence 2, Appli
30	379.5	15.4	349	4	US-09-006-353A-13	Sequence 13, Appl
31	373	15.1	355	1	US-08-292-549-6	Sequence 6, Appli
32	373	15.1	355	4	US-09-006-353A-14	Sequence 14, Appl
33	360.5	14.6	326	1	US-08-292-549-4	Sequence 4, Appli
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35	351.5	14.2	300	2	US-08-794-796-2	Sequence 2, Appli
36	343.5	13.9	605	4	US-09-042-785A-23	Sequence 23, Appl
37	343.5	13.9	655	3	US-08-959-382-2	Sequence 2, Appli
38	343.5	13.9	655	4	US-09-527-236A-2	Sequence 2, Appli
39	342	13.9	299	4	US-09-286-529-17	Sequence 17, Appl
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44	330	13.4	401	4	US-08-795-447A-6	Sequence 6, Appli
45	330	13.4	401	4	US-08-974-186-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-08-385-229-2
; Sequence 2, Application US/08385229
; Patent No. 5605690
; GENERAL INFORMATION:
;   APPLICANT: Jacobs, Cindy A.
;   APPLICANT: Smith, Craig A.
;   TITLE OF INVENTION: Method of Treating TNF-Dependent
;   TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Immunex Corporation
;     STREET: 51 University Street
;     CITY: Seattle
;     STATE: Washington
;     COUNTRY: U.S.A.
;     ZIP: 98101
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/385,229
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/07/946,236
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Wight, Christopher L.
;     REGISTRATION NUMBER: 31,680
;     REFERENCE/DOCKET NUMBER: 2503
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 587-0430
;     TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 461 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-385-229-2


  Query Match 100.0%; Score 2468; DB 1; Length 461;
  Best Local Similarity 100.0%; Pred. No. 5.7e-173;
  Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
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Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

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Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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; Sequence 2, Application US/08650000
; Patent No. 5945397
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Craig A.
;    APPLICANT:  Goodwin, Raymond G.
;    APPLICANT:  Beckmann, M. Patricia
;    TITLE OF INVENTION:  Tumor Necrosis Factor Receptors
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/650,000
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,453
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/038,765
;      FILING DATE:
;      APPLICATION NUMBER:  US 403,241
;      FILING DATE:  05-SEP-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 405,370
;      FILING DATE:  11-SEP-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 421,417
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 523,635
;      FILING DATE:  10-MAY-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wight, Christopher L.
;      REGISTRATION NUMBER:  31,680
;      REFERENCE/DOCKET NUMBER:  2501-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-650-000-2


  Query Match           100.0%;  Score 2468;  DB 2;  Length 461;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-173;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

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; Sequence 3, Application US/08477347
; Patent No. 6232446
;  GENERAL INFORMATION:
;    APPLICANT:  WALLACH, David
;    APPLICANT:  BIGDA, Jacek
;    APPLICANT:  BELETSKY, Igor
;    APPLICANT:  METT, Igor
;    TITLE OF INVENTION:  TNF LIGANDS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/477,347
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/115,685
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  IL 106271
;       FILING DATE:  08-JUL-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Townsend, G. Kevin
;       REGISTRATION NUMBER:  34,033
;       REFERENCE/DOCKET NUMBER:  WALLACH=10
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;       TELEX:  248633
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  461 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-477-347-3


  Query Match             100.0%;  Score 2468;  DB 4;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-173;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
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Db      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
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RESULT   4
US-08-476-862-2
; Sequence 2, Application US/08476862
; Patent No. 6262239
;  GENERAL INFORMATION:
;     APPLICANT:  WALLACH, David
;     APPLICANT:  BIGDA, Jacek
;     APPLICANT:  BELETSKY, Igor
;     APPLICANT:  METT, Igor
;     APPLICANT:  ENGELMANN, Hartmut
;     TITLE OF INVENTION:  TNF INHIBITORS
;     NUMBER OF SEQUENCES:  8
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/476,862
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  IL 107267
;       FILING DATE:  12-OCT-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  IL 94039
;       FILING DATE:  06-APR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  IL 91229
;       FILING DATE:  06-AUG-1989
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  IL 90339
;       FILING DATE:  18-MAY-1989
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  WALLACH=12A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  461 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-476-862-2


  Query Match             100.0%;  Score 2468;  DB 4;  Length 461;
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  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
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Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
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Db    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461


RESULT   5
5395760-2
;Patent No. 5395760
;    APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
;M. PATRICIA
;    TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
;B-RECEPTORS
;    NUMBER OF SEQUENCES: 17
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/523,635
;      FILING DATE: 10-MAY-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 421,417
;      FILING DATE: 13-OCT-1989
;      APPLICATION NUMBER: 405,370
;      FILING DATE: 11-SEP-1989
;      APPLICATION NUMBER: 403,241
;      FILING DATE: 05-SEP-1989
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;      LENGTH: 461
5395760-2


  Query Match             100.0%;  Score 2468;  DB 6;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-173;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||||
Db    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461


RESULT   6
US-09-042-785A-7
; Sequence 7, Application US/09042785A
; Patent No. 6194151
;  GENERAL INFORMATION:
;    APPLICANT:  Busfield, Samantha J
;    TITLE OF INVENTION:  NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,785A
;      FILING DATE:  17-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/938,896
;      FILING DATE:  26-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MEI-001CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-042-785A-7


  Query Match             99.8%;  Score 2462;  DB 4;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-172;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
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Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||
Db    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461


RESULT   7
US-09-006-353A-4
; Sequence 4, Application US/09006353A
; Patent No. 6261801
;  GENERAL INFORMATION:
;    APPLICANT:  WEI, YING-FEI
;    APPLICANT:  YU, GUO-LIANG
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  RUBEN, STEVEN
;    TITLE OF INVENTION:  TUMOR NECROSIS FACTOR RECEPTOR 5
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
;      CITY:  ROCKVILLE
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,353A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROOKES, ANDERS A
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF341
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-006-353A-4


  Query Match             99.8%;  Score 2462;  DB 4;  Length 461;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-172;
  Matches  460;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGVEASGAGE 360

Qy    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQ 420

Qy    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          |||||||||||||||||||||||||||||||||||||||||
Db    421 VPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461


RESULT   8
US-08-650-000-4
; Sequence 4, Application US/08650000
; Patent No. 5945397
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Craig A.
;    APPLICANT:  Goodwin, Raymond G.
;    APPLICANT:  Beckmann, M. Patricia
;    TITLE OF INVENTION:  Tumor Necrosis Factor Receptors
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/650,000
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,453
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/038,765
;      FILING DATE:
;      APPLICATION NUMBER:  US 403,241
;      FILING DATE:  05-SEP-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 405,370
;      FILING DATE:  11-SEP-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 421,417
;      FILING DATE:  13-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 523,635
;      FILING DATE:  10-MAY-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wight, Christopher L.
;      REGISTRATION NUMBER:  31,680
;      REFERENCE/DOCKET NUMBER:  2501-D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  474 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-650-000-4

Query Match 61.3%; Score 1512; DB 2; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

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Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
Db       1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy      60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
Db      61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120

Qy     120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
Db     121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180

Qy     179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
Db     181 CRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP- 239

Qy     239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
Db     240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQRKKKPSCLQRD 298

Qy     298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
Db     299 AKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQ 358

Qy     357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
Db     359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 418

Qy     417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
Db     419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461
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RESULT 9
US-09-042-785A-8
; Sequence 8, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
;   APPLICANT: Busfield, Samantha J
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
;   TITLE OF INVENTION: AND USES THEREFOR
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD, LLP
;     STREET: 28 State Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/042,785A
;     FILING DATE: 17-MAR-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/938,896
;     FILING DATE: 26-SEP-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mandragouras, Amy E
;     REGISTRATION NUMBER: 36,207
;     REFERENCE/DOCKET NUMBER: MEI-001CP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 474 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: internal
US-09-042-785A-8
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Query Match 61.3%; Score 1512; DB 4; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;
Matches 293; Conservative 50; Mismatches 114; Indels 8; Gaps 6;

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Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
Db       1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy      60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
Db      61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120

Qy     120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
Db     121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180

Qy     179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
Db     181 CRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP- 239

Qy     239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
Db     240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQRKKKPSCLQRD 298

Qy     298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
Db     299 AKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQ 358

Qy     357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
Db     359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 418

Qy     417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
Db     419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461
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RESULT 10
5395760-4
;Patent No. 5395760
;   APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
;M. PATRICIA
;   TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
;B-RECEPTORS
;   NUMBER OF SEQUENCES: 17
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/523,635
;     FILING DATE: 10-MAY-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 421,417
;     FILING DATE: 13-OCT-1989
;     APPLICATION NUMBER: 405,370
;     FILING DATE: 11-SEP-1989
;     APPLICATION NUMBER: 403,241
;     FILING DATE: 05-SEP-1989
;SEQ ID NO:4:
;     LENGTH: 474
5395760-4
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Query Match 61.3%; Score 1512; DB 6; Length 474;
Best Local Similarity 63.0%; Pred. No. 4.7e-103;

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  Matches  293;  Conservative   50;  Mismatches  114;  Indels    8;  Gaps    6;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRL-REYYDQTAQMCCSKCSP 59
          ||| |:| ||   |:|||  | :|||| ||| |||| |:: :|||: |||||:|| |
Db      1 MAPAALWVALVFELQLWATGHTVPAQVVLTPYKPEPGYECQISQEYYDRKAQMCCAKCPP 60

Qy     60 GQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICT 119
          ||: | || |||||||  || | |||:||    |||| | |::|||| :|||::|||:|
Db     61 GQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCA 120

Qy    120 CRPGWYCALSKQEG-CRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI 178
          |  | ||||    | || |  | || ||||||       :|:|| |||||||:||||||:
Db    121 CEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTFSDTTSSTDV 180

Qy    179 CRPHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPS 238
          ||||:||:::|||||| ||||   ||| |  |  ::: ||  ||||     | ||  |
Db    181 CRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTP- 239

Qy    239 TSFLLPMGPSPPAEGST-GDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQRE 297
           | |  :| :|  | || |  :||:|||||||:||||::|:|||:|: | |||| ||||:
Db    240 -SILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCIILVQRKKKPSCLQRD 298

Qy    298 AKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAPTRNQPQAPGV-EAS 356
          |||||:| :|::   | |||||| ||||||||||||||| |||||    |||  : ||
Db    299 AKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHPQARVMAEAQ 358

Qy    357 GAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESP 416
          |  ||||||  |||| | ||| ||||||||||||||||||||:|:|| |: || ||
Db    359 GFQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATVGDPDAKPSASP 418

Qy    417 KDEQVPFSKEECAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS 461
          ||||||||:|||  :|  || |||   : ||||||||| |||||
Db    419 KDEQVPFSQEECPSQSPCETTETL--QSHEKPLPLGVPDMGMKPS 461


RESULT  11
US-08-385-229-4
; Sequence 4, Application US/08385229
; Patent No. 5605690
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Cindy A.
;    APPLICANT:  Smith, Craig A.
;    TITLE OF INVENTION:  Method of Treating TNF-Dependent
;    TITLE OF INVENTION:  Inflammation Using Tumor Necrosis Factor Antagonists
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,229
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,236
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wight, Christopher L.
;      REGISTRATION NUMBER:  31,680
;      REFERENCE/DOCKET NUMBER:  2503
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 587-0606
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  518 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-385-229-4


  Query Match           58.1%;  Score 1433;  DB 1;  Length 518;
  Best Local Similarity   64.5%;  Pred. No. 3.1e-97;
  Matches  289;  Conservative   22;  Mismatches   67;  Indels   70;  Gaps   10;

Qy      1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     30 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 89

Qy     61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     90 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 149

Qy    121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    150 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 209

Qy    181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    210 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 269

Qy    241 FLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMTQVKKKPLCLQREAKV 300
          ||||||||||||||||                                    :|    :
Db    270 FLLPMGPSPPAEGSTGD-------------------------------EPKSCDKTHTC 297

Qy    301 PHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALDRRAP---------TRNQPQ-- 349
          |  || :  |  ||     :  |     :|  |      | |          :   |:
Db    298 PPCPAPELLG--GPS----VFLFPPKPKDTLMIS------RTPEVTCVVVDVSHEDPEVK 345

Qy    350 ----APGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNV--CSSSDHSSQCSSQA-S 402
              |||       | |   :         |:|  :::    :  |:  : |::|
Db    346 FNWYVDGVEVH-----NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKDYKCKVSNKALP 400

Qy    403 STMGDTDSSPSESPKDEQV---PFSKEE 427
          : |  | |     |:: ||   | |::|
Db    401 APMQKTISKAKGQPREPQVYTLPPSRDE 428


RESULT  12
US-08-243-010-1
; Sequence 1, Application US/08243010
; Patent No. 5639597
;  GENERAL INFORMATION:
;    APPLICANT:  Lauffer, Leander
;    APPLICANT:  Zettlmeissel, Gerd
;    APPLICANT:  Oquendo, Patricia
;    TITLE OF INVENTION:  Cell-free Receptor Binding Assays, The
;    TITLE OF INVENTION:  Production and Use Thereof
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/243,010
;      FILING DATE:  13-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  US 07/798,564
;      FILING DATE:  26-NOV-1991
;      APPLICATION NUMBER:  DE P 40 37 837.3
;      FILING DATE:  28-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Einaudi, Carol P.
;      REGISTRATION NUMBER:  32,220
;      REFERENCE/DOCKET NUMBER:  02481-1132-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  486 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-243-010-1


  Query Match             56.9%;  Score 1404;  DB 1;  Length 486;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-95;
  Matches  252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 240

Qy     241 FLLPMGPSPPAE 252
           ||||||||||||
Db     241 FLLPMGPSPPAE 252


RESULT  13
US-09-326-394-4
; Sequence 4, Application US/09326394
; Patent No. 6306820
;  GENERAL INFORMATION:
;    APPLICANT:  Bendele, Alison M.
;    APPLICANT:  Sennello, Regina M.
;    APPLICANT:  Edwards, Carl K.
;    TITLE OF INVENTION:  COMBINATION THERAPY USING A TNF BINDING
;    TITLE OF INVENTION:  PROTEIN FOR TREATING TNF-MEDIATED DISEASES
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 DeHavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/326,394
;      FILING DATE:  08-DEC-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,587
;      FILING DATE:  06-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/036,355
;      FILING DATE:  23-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,315
;      FILING DATE:  07-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/052,023
;      FILING DATE:  09-JUL-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zindrick, Thomas K.
;      REGISTRATION NUMBER:  32,185
;      REFERENCE/DOCKET NUMBER:  A-430D
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  235 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-326-394-4


  Query Match             53.2%;  Score 1312;  DB 4;  Length 235;
  Best Local Similarity   99.6%;  Pred. No. 8.2e-89;
  Matches  234;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      23 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 82
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 LPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDST 60

Qy      83 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRK 120

Qy     143 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDAVCTS 202
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     121 CRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASRDAVCTS 180

Qy     203 TSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD 257
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD 235


RESULT  14
US-08-974-022-48
; Sequence 48, Application US/08974022
; Patent No. 6015938
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,022
;      FILING DATE:  12-DEC-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-974-022-48


  Query Match             51.2%;  Score 1263;  DB 3;  Length 227;
  Best Local Similarity   99.6%;  Pred. No. 3e-85;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227
           ||||||||||||||| ||||||||||||||||||||||||||||||
Db     181 PHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227


RESULT  15
US-08-795-445A-48
; Sequence 48, Application US/08795445A
; Patent No. 6284485
;  GENERAL INFORMATION:
;    APPLICANT:  Boyle, Willaim J.
;    APPLICANT:  Lacey, David L.
;    APPLICANT:  Calzone, Frank J.
;    APPLICANT:  Chang, Ming-Shi
;    TITLE OF INVENTION:  OSTEOPROTEGERIN
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  91320-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,445A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/577,788
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Winter, Robert B.
;      REFERENCE/DOCKET NUMBER:  A-378
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  227 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-445A-48


  Query Match             51.2%;  Score 1263;  DB 4;  Length 227;
  Best Local Similarity   99.6%;  Pred. No. 3e-85;
  Matches  226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy     181 PHQICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227
           ||||||||||||||| ||||||||||||||||||||||||||||||
Db     181 PHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHT 227


Search completed: August 21, 2002, 09:54:05
Job time: 53 sec
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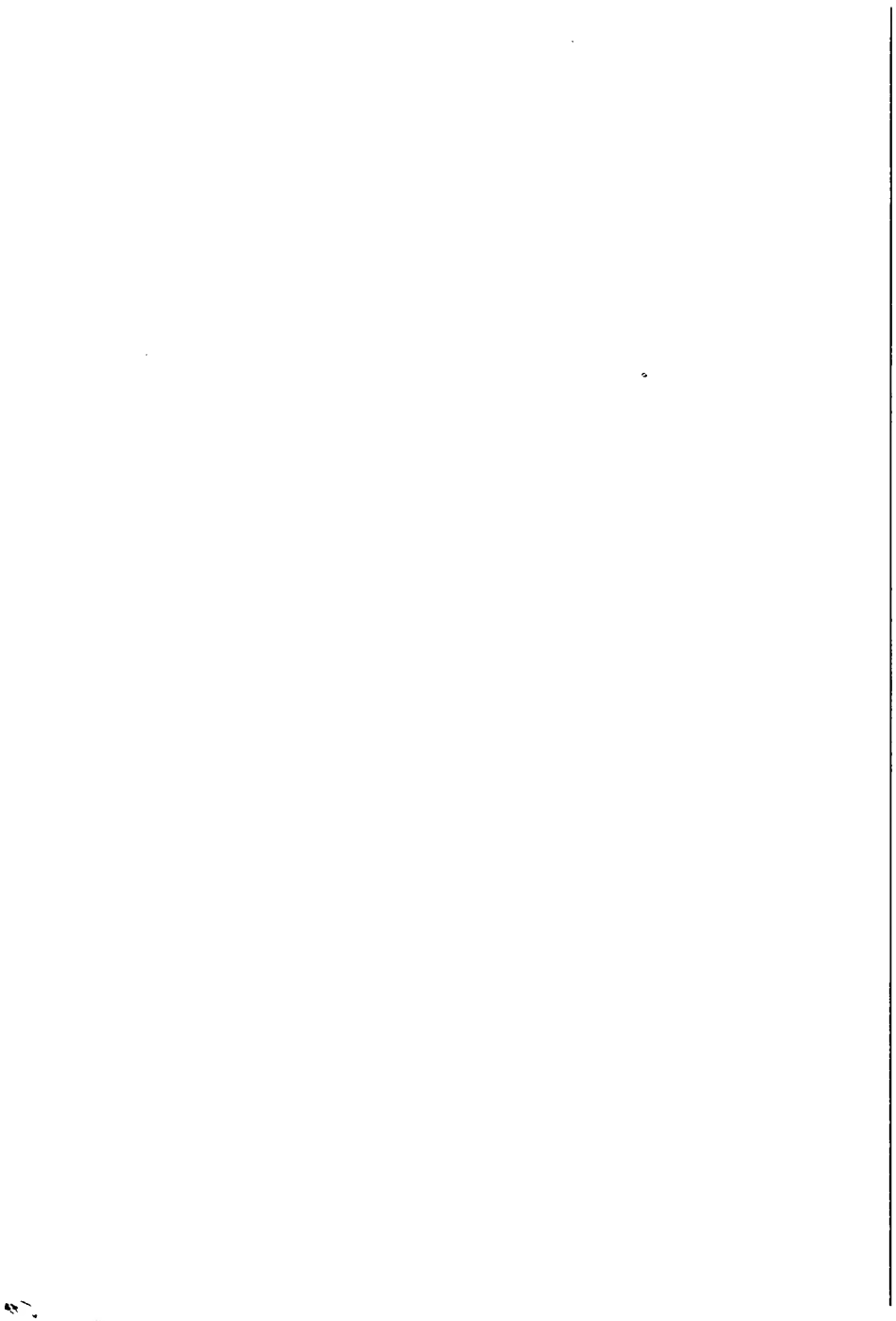

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:05:57 ; Search time 57.9 Seconds
(without alignments)
94.596 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 14670

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	23.5	54	2	A60726	mucin, gallbladder
2	56.5	18.7	52	2	S63324	hypothetical prote
3	55.5	18.4	42	2	I70082	glycoprotein Ib al
4	51	16.9	25	2	I40692	cenA protein (IgA1
5	50	16.6	46	2	S07073	arabinogalactan pr
6	47	15.6	31	2	T36022	small hypothetical
7	44.5	14.7	57	2	S10782	salivary protein P
8	44.5	14.7	57	2	S16587	hypothetical prote
9	44	14.6	28	2	I56139	MHC class I HLA-J
10	43.5	14.4	47	2	S32108	sepiapterin reduct
11	43.5	14.4	54	2	D81737	hypothetical prote
12	43	14.2	31	2	I54515	pre-B cell Ig lamb
13	43	14.2	39	2	A46662	collagen alpha 2(V
14	42	13.9	36	2	A37172	collagen alpha 1(X
15	42	13.9	48	2	I46522	troponin T 2fa - r
16	42	13.9	50	2	AH2135	hypothetical prote
17	42	13.9	55	2	S08424	H+-transporting AT
18	42	13.9	55	2	T11184	H+-transporting AT
19	41	13.6	42	2	T07030	extensin - tomato
20	40.5	13.4	50	2	A29789	mucin - sheep (fra
21	40	13.2	29	2	G39690	neural cell adhesi
22	40	13.2	50	2	H64801	hypothetical prote
23	40	13.2	51	2	A33756	dorsal protein - f
24	40	13.2	51	2	G72801	gp18 protein - Myc
25	40	13.2	52	2	S58216	hypothetical prote
26	40	13.2	54	2	T11131	ATP synthase subun
27	40	13.2	55	2	T11105	H+-transporting AT
28	40	13.2	57	2	I58120	gene insl protein
29	39.5	13.1	52	2	S01945	myosin catalytic l
30	39	12.9	27	2	S51176	aspartate transcar
31	39	12.9	53	2	S17672	hypothetical prote
32	38.5	12.7	51	2	C81117	hypothetical prote
33	38	12.6	53	2	S23202	kappa-casein - bov
34	38	12.6	54	2	S14338	serpin I - horse (
35	38	12.6	55	2	S29770	DNA-binding protei
36	38	12.6	55	2	A37238	autoimmune epitope
37	37.5	12.4	49	2	S25433	neural cell adhesi
38	37.5	12.4	51	2	T29481	hypothetical prote
39	37.5	12.4	57	2	E41715	hypothetical prote
40	37.5	12.4	57	2	T36648	hypothetical prote
41	37	12.3	30	2	JC1360	hypothetical 3K pr
42	37	12.3	38	2	S68260	hypothetical prote
43	37	12.3	42	2	A99578	lipoprotein vsaH [
44	37	12.3	45	2	S24713	Ig alpha chain, tr
45	37	12.3	49	2	S72213	beta-fructofuranos

ALIGNMENTS

RESULT 1
A60726
mucin, gallbladder - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 30-Sep-1993
C;Accession: A60726
R;Afdhal, N.H.; Offner, G.D.; Smith, B.F.
Gastroenterology 99, 1493-1501, 1990
A;Title: Characterization of bovine gallbladder mucin. Amino acid sequences of trypti
A;Reference number: A60726; MUID:91007106
A;Accession: A60726
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-54 <AFD>

Query Match 23.5%; Score 71; DB 2; Length 54;
Best Local Similarity 35.2%; Pred. No. 3;
Matches 19; Conservative 6; Mismatches 25; Indels 4; Gaps 2;

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Qy       2 STSPTRSMAPGAVHLPQPVSTRSQHT-QPTPEPSTAPSTSF---LLPMGPSPPA 51
           :|:|| :  ||:     | |:    |  ||  | | |  |      | || ||:
Db       1 TTTPTVTPLPGSPQTTTPTSSPLPETPTPTSTPPTVPGPSSPQDTEPSGPQPPS 54
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RESULT 2
S63324
hypothetical protein YNL338w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0170
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 05-Nov-1999
C;Accession: S63324
R;Obermaier, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63317
A;Accession: S63324
A;Molecule type: DNA
A;Residues: 1-52 <OBE>
A;Cross-references: EMBL:Z71614; NID:g1302466; PID:e239576; PID:g1302467; GSPDB:GN000
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNL338w
A;Map position: 14L

Query Match 18.7%; Score 56.5; DB 2; Length 52;
Best Local Similarity 35.7%; Pred. No. 55;
Matches 15; Conservative 4; Mismatches 20; Indels 3; Gaps 2;

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Qy       8 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           ||    :::| |  |   || ||| |   | |       |:|
Db      11 SMQYSDIYIPTPTPTHHTHT-PTPHPH--PHTHTHTHHNPNP 49
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```
RESULT   3
I70082
glycoprotein Ib alpha variant B - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C;Accession: I70082
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
ations.
A;Reference number: I55355; MUID:92250564
A;Accession: I70082
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-42 <RES>
A;Cross-references: GB:S34439; NID:g249178; PIDN:AAB22153.1; PID:g249179
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
C;Keywords: glycoprotein


  Query Match             18.4%;  Score 55.5;  DB 2;  Length 42;
  Best Local Similarity   35.6%;  Pred. No. 54;
  Matches   16;  Conservative    6;  Mismatches   18;  Indels    5;  Gaps    3;

Qy      5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
          ||   ||     |:| |  :  :  ||||:: |: |   |  | |
Db      2 PTSEPAPSPT-TPEPTSEPAP-SPTTPEPTSEPAPS---PTTPEP 41


RESULT   4
I40692
cenA protein (IgA1h) - Cellulomonas fimi (fragment)
C;Species: Cellulomonas fimi
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C;Accession: I40692
R;Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren
FEMS Microbiol. Lett. 92, 199-204, 1992
A;Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
hoeae.
A;Reference number: I40692
A;Accession: I40692
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-25 <RES>
A;Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036


  Query Match             16.9%;  Score 51;  DB 2;  Length 25;
  Best Local Similarity   46.2%;  Pred. No. 79;
  Matches   12;  Conservative    1;  Mismatches    5;  Indels    8;  Gaps    1;

Qy     24 SQHTQPTPEPSTAPSTSFLLPMGPSP 49
          |  | ||| ||| |:        |||
Db      2 SVSTPPTPSPSTPPT--------PSP 19


RESULT   5
S07073
arabinogalactan protein - Italian ryegrass (fragments)
C;Species: Lolium multiflorum (Italian ryegrass)
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 05-Dec-1998
C;Accession: S07073
R;Gleeson, P.A.; McNamara, M.; Wettenhall, R.E.H.; Stone, B.A.; Fincher, G.B.
Biochem. J. 264, 857-862, 1989
A;Title: Characterization of the hydroxyproline-rich protein core of an arabinogalactan-
A;Reference number: S07073; MUID:90147544
A;Accession: S07073
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-46 <GLE>
A;Note: 19-His and 23-Leu were also found
C;Keywords: hydroxyproline
F;6,7,9,11,14,16,18,20,26,30,34,36,39/Modified site: hydroxyproline (Pro) #status exp


  Query Match             16.6%;  Score 50;  DB 2;  Length 46;
  Best Local Similarity   37.1%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    4;  Mismatches   16;  Indels    2;  Gaps    1;

Qy     17 PQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPA 51
          |   : ::    | || ||||  :      |||||
Db      6 PPAPAPKAPAPAPVPEASTAPVAA--PTTXPSPPA 38


RESULT   6
T36022
small hypothetical protein SCC54.09c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36022
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T36022
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <SEE>
A;Cross-references: EMBL:AL035591; PIDN:CAB38139.1; GSPDB:GN00070; SCOEDB:SCC54.09c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCC54.09c


  Query Match             15.6%;  Score 47;  DB 2;  Length 31;
  Best Local Similarity   30.4%;  Pred. No. 2.2e+02;
  Matches    7;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     19 PVSTRSQHTQPTPEPSTAPSTSF 41
          |:: |::  :| | |:    | |
Db      2 PLAARNEDNEPVPAPTWVTGTGF 24


RESULT   7
S10782
salivary protein P-B - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S10782
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a
A;Reference number: S10780; MUID:90336641
A;Accession: S10782
A;Molecule type: protein
A;Residues: 1-57 <STR>
C;Superfamily: proline-rich peptide P-B


  Query Match             14.7%;  Score 44.5;  DB 2;  Length 57;
  Best Local Similarity   28.8%;  Pred. No. 6.9e+02;
  Matches   15;  Conservative    2;  Mismatches   28;  Indels    7;  Gaps    2;

Qy      5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 56
          |     || :  |||         | | |   |       : | |||    |
Db      4 PRGPYPPGPLAPPQPFG--PGFVPPPPPPPYGPGR-----IPPPPAPYGPG 48


RESULT   8
S16587
hypothetical protein 1 - lamb's-quarters
C;Species: Chenopodium album (lamb's-quarters)
C;Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: S16587
R;Doerfel, P.; Weihe, A.; Dolferus, R.; Boerner, T.
```

Plant Mol. Biol. 17, 155-156, 1991
A;Title: DNA sequence of a mitochondrial plasmid from Chenopodium album.
A;Reference number: S16587; MUID:91329724
A;Accession: S16587
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-57 <DOE>
A;Cross-references: EMBL:X58911

Query Match 14.7%; Score 44.5; DB 2; Length 57;
Best Local Similarity 34.2%; Pred. No. 6.9e+02;
Matches 13; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

```
Qy      16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
           ||  : | :    | |:|| ||: :  | : |   | |
Db      21 LPWYLRTLTFRRVP-PDPSQAPNFNHSLSLNPPSAAVG 57
```

RESULT 9
I56139
MHC class I HLA-J antigen - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I56139; I72807
R;Messer, G.; Zemmour, J.; Orr, H.T.; Parham, P.; Weiss, E.H.; Girdlestone, J.
J. Immunol. 148, 4043-4053, 1992
A;Title: HLA-J, a second inactivated class I HLA gene related to HLA-G and HLA-A. Implic
A;Reference number: I56139; MUID:92291530
A;Accession: I56139
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: GB:M80468; NID:g188481; PIDN:AAA36306.1; PID:g188482
A;Accession: I72807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28 <RE2>
A;Cross-references: GB:M80469; NID:g188483; PIDN:AAA36307.1; PID:g188484
C;Genetics:
A;Introns: 24/3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 14.6%; Score 44; DB 2; Length 28;
Best Local Similarity 40.9%; Pred. No. 3.7e+02;
Matches 9; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

```
Qy      17 PQPVSTRSQHTQPTPEPSTAPS 38
           |:| |  |:   | | |  ||:
Db       6 PEPSSCCSRGPWPWPRPGRAPT 27
```

RESULT 10
S32108
sepiapterin reductase (EC 1.1.1.153) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Sep-1997
C;Accession: S32108
R;Maier, J.
submitted to the EMBL Data Library, March 1993
A;Reference number: S32108
A;Accession: S32108
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-47 <MAI>
A;Cross-references: EMBL:Z21947
C;Keywords: oxidoreductase

Query Match 14.4%; Score 43.5; DB 2; Length 47;
Best Local Similarity 39.3%; Pred. No. 6.9e+02;
Matches 11; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

```
Qy      20 VSTRSQHTQPTPEPSTAPSTSFLLPMGP 47
           ||    |: | | | |: |    | :||
Db      14 VSGLKSHSPPAPHP-TSTSAVCSLTLGP 40
```

RESULT 11
D81737
hypothetical protein TC0127 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: D81737
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Accession: D81737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-54 <TET>
A;Cross-references: GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF39005.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0127

Query Match 14.4%; Score 43.5; DB 2; Length 54;
Best Local Similarity 42.9%; Pred. No. 7.9e+02;
Matches 12; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

```
Qy      28 QPTPEPSTAPSTSFLLPMGPSPPAEGST 55
           ||: :|| | | | |    |:||:  :|
Db       4 QPSKKPSQASSLS-LKGGDPAPPSGRAT 30
```

RESULT 12
I54515
pre-B cell Ig lambda-like omega light chain (non-rearranging) IGLL2 - human (fragment
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 23-Jul-1999
C;Accession: I54515
R;Bauer, T.R.; McDermid, H.E.; Budarf, M.L.; Van Keuren, M.L.; Blomberg, B.B.
Immunogenetics 38, 387-399, 1993
A;Title: Physical location of the human immunoglobulin lambda-like genes, 14.1, 16.1,
A;Reference number: I54515; MUID:94011089
A;Accession: I54515
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-31 <RES>
A;Cross-references: GB:L02326; NID:g292400; PIDN:AAA16174.1; PID:g451281
C;Genetics:
A;Gene: GDB:IGLL2
A;Cross-references: GDB:137325
A;Map position: 22q11.2-22q11.2
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 14.2%; Score 43; DB 2; Length 31;
Best Local Similarity 37.5%; Pred. No. 5e+02;
Matches 9; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

```
Qy      32 EPSTAPSTSFLLPMGPSPPAEGST 55
           :| | ||    ||    | |  :|
Db       2 QPKTTPSVILFLPSCEEPQANKAT 25
```

RESULT 13
A46662
collagen alpha 2(V) chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-1995
C;Accession: A46662

```
R;Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.
J. Biol. Chem. 268, 9381-9386, 1993
A;Title: Isolation and characterization of the chains of type V/type XI collagen present
A;Reference number: A46662; MUID:93252802
A;Accession: A46662
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-39 <MAY>
A;Experimental source: vitreous humor
A;Note: sequence extracted from NCBI backbone (NCBIP:131547)
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;


  Query Match             14.2%;  Score 43;  DB 2;  Length 39;
  Best Local Similarity   53.3%;  Pred. No. 6.3e+02;
  Matches    8;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      43 LPMGPSPPAEGSTGD 57
           ||  | || |   ||
Db      14 LPGPPGPPGEAGPGD 28


RESULT  14
A37172
collagen alpha 1(XII) chain-like, skin and tendon - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 19-Oct-1995
C;Accession: A37172
R;Dublet, B.; Van Der Rest, M.
Ann. N. Y. Acad. Sci. 580, 436-439, 1989
A;Title: Comparison between chicken type XII collagen and bovine homologues.
A;Reference number: A37172
A;Accession: A37172
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-36 <DUB>


  Query Match             13.9%;  Score 42;  DB 2;  Length 36;
  Best Local Similarity   41.4%;  Pred. No. 7.1e+02;
  Matches   12;  Conservative    3;  Mismatches    8;  Indels    6;  Gaps    3;

Qy      25 QHTQPTPEPSTA-PSTSFLLPMGPSPPAE 52
           |   | |:|: | ||     |  |||| :
Db       3 QERSP-PQPANAVPSX----PASPSPPLQ 26


RESULT  15
I46522
troponin T 2fa - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
C;Accession: I46522
R;Briggs, M.M.; Lin, J.J.; Schachat, F.H.
J. Muscle Res. Cell. Motil. 8, 1-12, 1987
A;Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle tropo
A;Reference number: I46522; MUID:87251333
A;Accession: I46522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-48 <BRI>
A;Cross-references: EMBL:U04975; NID:g440810; PIDN:AAA16028.1; PID:g440811
C;Superfamily: troponin T


  Query Match             13.9%;  Score 42;  DB 2;  Length 48;
  Best Local Similarity   37.9%;  Pred. No. 9.5e+02;
  Matches   11;  Conservative    3;  Mismatches    9;  Indels    6;  Gaps    2;

Qy      10 APGAVHLPQPVSTRSQHTQPTPEPS-TAP 37
           :|  || |: |     | :  | |  |||
Db      25 SPAEVHEPEEV-----HEEEKPRPKLTAP 48
```

Search completed: August 21, 2002, 10:08:50
Job time: 173 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:07:47 ; Search time 10.26 Seconds
(without alignments)
215.109 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 4574

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	56.5	18.7	52	1	YN78_YEAST	P53820 saccharomyc
2	44.5	14.7	57	1	PRPB_HUMAN	P02814 homo sapien
3	42	13.9	55	1	ATP8_GADMO	P15996 gadus morhu
4	40	13.2	51	1	VG18_BPMD2	O64211 mycobacteri
5	40	13.2	55	1	ATP8_PELSU	O79674 pelomedusa
6	39	12.9	56	1	TA6P_HUMAN	Q9y3f1 homo sapien
7	38	12.6	51	1	MLEV_MOUSE	P09542 mus musculu
8	38	12.6	55	1	ATP8_PAROL	Q9t9d5 paralichthy
9	37.5	12.4	16	1	FOR2_MYRGU	P81437 myrmecia gu
10	37.5	12.4	57	1	RPOK_HALMA	P29200 haloarcula
11	36.5	12.1	55	1	YPU3_RHOCA	P26159 rhodobacter
12	36	11.9	30	1	AP65_CARMA	P82964 carcinus ma
13	36	11.9	55	1	ATP8_SQUAC	Q9zz50 squalus aca
14	35	11.6	51	1	INE1_HUMAN	O15225 homo sapien
15	35	11.6	53	1	CA11_RABIT	P02456 oryctolagus
16	35	11.6	55	1	ATP8_SALAL	Q9xn27 salvelinus
17	34.5	11.4	16	1	FOR1_MYRGU	P81438 myrmecia gu
18	34.5	11.4	52	1	Y180_TREPA	O83210 treponema p
19	34	11.3	55	1	ATP8_RHEAM	O79396 rhea americ
20	34	11.3	55	1	M84C_DROME	Q01644 drosophila
21	33.5	11.1	38	1	H5_COLLI	P02260 columba liv
22	33.5	11.1	52	1	MTK_DROME	Q24395 drosophila
23	33.5	11.1	52	1	PH68_HUMAN	Q9uht9 homo sapien
24	33.5	11.1	55	1	ATP8_AYTAM	Q9xkz5 aythya amer
25	33	10.9	32	1	CAPP_METEX	Q49136 methylobact
26	33	10.9	33	1	PBAN_LYMDI	P43511 lymantria d
27	33	10.9	50	1	ZNT4_BOVIN	Q9ttf3 bos taurus
28	33	10.9	51	1	TAT_HV1J3	P12508 human immun
29	33	10.9	54	1	ATP8_CARAU	O78683 carassius a
30	33	10.9	54	1	ATP8_CYPCA	P24948 cyprinus ca
31	33	10.9	55	1	ATP8_LOXNO	Q9mdj1 loxigilla n
32	32	10.6	34	1	RNL1_PIG	P15466 sus scrofa
33	32	10.6	50	1	SPRT_RAT	P81728 rattus norv
34	32	10.6	55	1	ATP8_LATCH	O03168 latimeria c
35	32	10.6	55	1	ATP8_SALFO	Q9xn35 salvelinus
36	31.5	10.4	17	1	A45K_MYCBO	P80069 mycobacteri
37	31.5	10.4	55	1	ATP8_STRCA	O21401 struthio ca
38	31	10.3	20	1	DFTS_RAT	P07448 rattus norv
39	31	10.3	20	1	UCRQ_EQUAR	P81247 equisetum a
40	31	10.3	46	1	YPC4_ECOLI	P19755 escherichia
41	31	10.3	55	1	ATP8_CROLA	P34190 crossostoma
42	30.5	10.1	50	1	PEN1_PENVA	P81056 penaeus van
43	30.5	10.1	52	1	RUBR_DESVH	P00269 desulfovibr
44	30.5	10.1	55	1	A70A_DROSE	O18417 drosophila
45	30	9.9	26	1	CATG_RAT	P17977 rattus norv

ALIGNMENTS

RESULT 1
YN78_YEAST
ID YN78_YEAST STANDARD; PRT; 52 AA.
AC P53820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 6.0 kDa protein in COS1 5'region.
GN YNL338W OR N0170.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: TO YEAST YHR217C.
CC ---
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; Z71614; CAA96274.1; -.
DR EMBL; Z71613; CAA96273.1; -.
DR SGD; S0005282; YNL338W.
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5951 MW; C1E4066D43E057A1 CRC64;

Query Match 18.7%; Score 56.5; DB 1; Length 52;
Best Local Similarity 35.7%; Pred. No. 32;
Matches 15; Conservative 4; Mismatches 20; Indels 3; Gaps 2;

```
Qy       8 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           ||    :::| |  |   || ||| |   | |       |:|
Db      11 SMQYSDIYIPTPTPTHHTHT-PTPHPH--PHTHTHTHHNPNP 49
```

RESULT 2
PRPB_HUMAN
ID PRPB_HUMAN STANDARD; PRT; 57 AA.
AC P02814;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proline-rich peptide P-B [Contains: Peptide P-A].
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```
RP   SEQUENCE.
RC   TISSUE=Saliva;
RX   MEDLINE=80006513; PubMed=479131;
RA   Isemura S., Saitoh E., Sanada K.;
RT   "Isolation and amino acid sequences of proline-rich peptides of human
RT   whole saliva.";
RL   J. Biochem. 86:79-86(1979).
CC   -!- PTM: P-A IS PROBABLY A DEGRADATION PRODUCT OF P-B.
DR   PIR; A03297; PJHUSB.
KW   Repeat; Saliva.
FT   CHAIN         1     57       PROLINE-RICH PEPTIDE P-B.
FT   CHAIN        20     57       PEPTIDE P-A.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
SQ   SEQUENCE   57 AA;  5810 MW;  2085FBB83BAFD063 CRC64;


  Query Match             14.7%;  Score 44.5;  DB 1;  Length 57;
  Best Local Similarity   28.8%;  Pred. No. 3.6e+02;
  Matches   15;  Conservative    2;  Mismatches   28;  Indels    7;  Gaps    2;

Qy       5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 56
           |     || :  |||         | | |   |       : | |||    |
Db       4 PRGPYPPGPLAPPQPFG--PGFVPPPPPPPYGPGR-----IPPPPPAPYGPG 48


RESULT   3
ATP8_GADMO
ID   ATP8_GADMO     STANDARD;      PRT;    55 AA.
AC   P15996;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN   MTATP8 OR ATP8.
OS   Gadus morhua (Atlantic cod).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
OC   Gadus.
OX   NCBI_TaxID=8049;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NORWEGIAN COASTAL 1; TISSUE=Liver;
RX   MEDLINE=90174958; PubMed=2308841;
RA   Johansen S., Guddal P.H., Johansen T.;
RT   "Organization of the mitochondrial genome of Atlantic cod, Gadus
RT   morhua.";
RL   Nucleic Acids Res. 18:411-419(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NORWEGIAN COASTAL 1;
RX   MEDLINE=96414925; PubMed=8817926;
RA   Johansen S., Bakke I.;
RT   "The complete mitochondrial DNA sequence of Atlantic cod (Gadus
RT   morhua): relevance to taxonomic studies among codfishes.";
RL   Mol. Mar. Biol. Biotechnol. 5:203-214(1996).
CC   -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC       (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X17659; CAA35655.1; -.
DR   EMBL; X99772; CAA68110.1; -.
DR   PIR; S08424; S08424.
DR   InterPro; IPR001421; ATP-synt_8.
DR   Pfam; PF00895; ATP-synt_8; 1.
KW   Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT   TRANSMEM      4     24       POTENTIAL.
SQ   SEQUENCE   55 AA;  6481 MW;  E85C81E63DB48B15 CRC64;


  Query Match             13.9%;  Score 42;  DB 1;  Length 55;
  Best Local Similarity   32.0%;  Pred. No. 5.7e+02;
  Matches    8;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      16 LPQPVSTRSQHTQPTPEPSTAPSTS 40
           ||  |   :   :|:|:  | | |:
Db      24 LPPKVMAHTFPNEPSPQGMTTPKTA 48


RESULT   4
VG18_BPMD2
ID   VG18_BPMD2     STANDARD;      PRT;    51 AA.
AC   O64211;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Gene 18 protein (GP18).
GN   18.
OS   Mycobacteriophage D29.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=28369;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98300335; PubMed=9636706;
RA   Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT   "Genome structure of mycobacteriophage D29: implications for phage
RT   evolution.";
RL   J. Mol. Biol. 279:143-164(1998).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF022214; AAC18458.1; -.
SQ   SEQUENCE   51 AA;  5680 MW;  EF85B1AFF5786A34 CRC64;


  Query Match             13.2%;  Score 40;  DB 1;  Length 51;
  Best Local Similarity   33.3%;  Pred. No. 7.8e+02;
  Matches   11;  Conservative    4;  Mismatches   14;  Indels    4;  Gaps    1;

Qy       7 RSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST 39
           | :| |    |:   |    |:| | |   |:|
Db      21 RLIAAGGWKRPRKPRT----TKPKPAPKQEPAT 49


RESULT   5
ATP8_PELSU
ID   ATP8_PELSU     STANDARD;      PRT;    55 AA.
AC   O79674;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN   MTATP8 OR ATP8.
OS   Pelomedusa subrufa (African side-necked turtle).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Pleurodira; Pelomedusidae; Pelomedusa.
OX   NCBI_TaxID=44522;
RN   [1]
RP   SEQUENCE FROM N.A.
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RA   Zardoya R.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC       (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF039066; AAD05054.1; -.
DR   InterPro; IPR001421; ATP-synt_8.
DR   Pfam; PF00895; ATP-synt_8; 1.
KW   Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT   TRANSMEM      4     24       POTENTIAL.
SQ   SEQUENCE   55 AA;  6536 MW;  D8D4BC8F8651A001 CRC64;


  Query Match             13.2%;  Score 40;  DB 1;  Length 55;
  Best Local Similarity   36.0%;  Pred. No. 8.4e+02;
  Matches    9;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

Qy      15 HLPQPVSTRSQHTQPTPEPSTAPST 39
           |:|    |  ::   || | | | |
Db      31 HIPNNSPTNKKNMLTTPMPWTWPWT 55


RESULT   6
TA6P_HUMAN
ID   TA6P_HUMAN     STANDARD;      PRT;    56 AA.
AC   Q9Y3F1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   TAP2-associated 6.5 kDa polypeptide.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li H.C.;
RT   "A 56 aa polypeptide with phosphorylation motif, potentially
RT   associated with Tap2 isoform activity.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE ASSOCIATED WITH TAP2 ISOFORM ACTIVITY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF152583; AAD32715.1; -.
SQ   SEQUENCE   56 AA;  6535 MW;  ACD5D223EEC2C3BA CRC64;


  Query Match             12.9%;  Score 39;  DB 1;  Length 56;
  Best Local Similarity   40.0%;  Pred. No. 1e+03;
  Matches    8;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      30 TPEPSTAPSTSFLLPMGPSP 49
           ||:  |    |::| : |||
Db       6 TPQILTISFVSYILSLFPSP 25


RESULT   7
MLEV_MOUSE
ID   MLEV_MOUSE     STANDARD;      PRT;    51 AA.
AC   P09542;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Myosin light chain 1, slow-twitch muscle B/ventricular isoform
DE   (Fragment).
GN   MYL3 OR MYLC OR MLC1V.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H; TISSUE=Spleen;
RX   MEDLINE=89057447; PubMed=3194193;
RA   Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
RA   Buckingham M.E.;
RT   "Promoter analysis of myosin alkali light chain genes expressed in
RT   mouse striated muscle.";
RL   Nucleic Acids Res. 16:10037-10052(1988).
CC   -!- SUBUNIT: MYOSIN IS A HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS.
CC   -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS, BUT THIS
CC       PROTEIN DOES NOT BIND CALCIUM.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X12972; CAA31415.1; -.
DR   MGD; MGI:97268; Mylc.
DR   PIR; S01945; S01945.
DR   HSSP; P04002; 1ATF.
KW   Myosin; Muscle protein; Multigene family.
FT   INIT_MET      0      0
FT   NON_TER      51     51
SQ   SEQUENCE   51 AA;  5085 MW;  CE513ECBA3C8258D CRC64;


  Query Match             12.6%;  Score 38;  DB 1;  Length 51;
  Best Local Similarity   26.3%;  Pred. No. 1.1e+03;
  Matches   10;  Conservative    6;  Mismatches   20;  Indels    2;  Gaps    1;

Qy      17 PQPVSTRSQHTQP--TPEPSTAPSTSFLLPMGPSPPAE 52
           |:|    ::   |   | |: ||: :      |  | |
Db       5 PEPKKDDAKAAAPKAAPAPAAAPAAAPAAAPEPERPKE 42


RESULT   8
ATP8_PAROL
ID   ATP8_PAROL     STANDARD;      PRT;    55 AA.
AC   Q9T9D5;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN   MTATP8 OR ATP8.
OS   Paralichthys olivaceus (Flounder).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Paralichthyidae; Paralichthys.
OX   NCBI_TaxID=8255;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Saitoh K., Hayashizaki K., Yokoyama Y., Asahida T., Toyohara H.,
```

```
RA   Yamashita Y.;
RT   "The complete nucleotide sequence of Japanese flounder mitochondrial
RT   genome: structural property and cue for resolving teleostean
RT   relationship.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC       (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB028664; BAA89037.1; -.
DR   InterPro; IPR001421; ATP-synt_8.
DR   Pfam; PF00895; ATP-synt_8; 1.
KW   Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
SQ   SEQUENCE   55 AA;  6571 MW;  2B5EFE20FDCB6AA9 CRC64;


  Query Match             12.6%;  Score 38;  DB 1;  Length 55;
  Best Local Similarity   29.2%;  Pred. No. 1.2e+03;
  Matches    7;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      16 LPQPVSTRSQHTQPTPEPSTAPST 39
           :|  |   :   :|||: :  | |
Db      24 IPPKVLAHTFPNEPTPQSTQKPKT 47


RESULT   9
FOR2_MYRGU
ID   FOR2_MYRGU     STANDARD;      PRT;    16 AA.
AC   P81437;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Formaecin 2.
OS   Myrmecia gulosa (Red bulldog ant).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC   Formicidae; Myrmeciinae; Myrmecia.
OX   NCBI_TaxID=36170;
RN   [1]
RP   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC   TISSUE=Hemolymph;
RX   MEDLINE=98165787; PubMed=9497332;
RA   Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT   "Isolation from an ant Myrmecia gulosa of two inducible
RT   O-glycosylated proline-rich antibacterial peptides.";
RL   J. Biol. Chem. 273:6139-6143(1998).
CC   -!- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI
CC       BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC       BACTERIA.
CC   -!- INDUCTION: By bacterial infection.
CC   -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
CC       GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC   -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
KW   Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
FT   CARBOHYD     11     11       O-LINKED (GALNAC. . .).
SQ   SEQUENCE   16 AA;  1807 MW;  9C3CA3B00BC2E0AE CRC64;


  Query Match             12.4%;  Score 37.5;  DB 1;  Length 16;
  Best Local Similarity   47.1%;  Pred. No. 4.1e+02;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    5;  Gaps    1;

Qy      17 PQPVSTRSQHTQPTPEP 33
           | ||:|:     ||| |

Db       3 PNPVNTK-----PTPYP 14


RESULT  10
RPOK_HALMA
ID   RPOK_HALMA     STANDARD;      PRT;    57 AA.
AC   P29200;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   DNA-directed RNA polymerase subunit K (EC 2.7.7.6).
GN   RPOK.
OS   Haloarcula marismortui (Halobacterium marismortui).
OC   Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloarcula.
OX   NCBI_TaxID=2238;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92105119; PubMed=1840597;
RA   Kroemer W.J., Arndt E.;
RT   "Halobacterial S9 operon. Three ribosomal protein genes are
RT   cotranscribed with genes encoding a tRNA(Leu), the enolase, and a
RT   putative membrane protein in the archaebacterium Haloarcula
RT   (Halobacterium) marismortui.";
RL   J. Biol. Chem. 266:24573-24579(1991).
RN   [2]
RP   SIMILARITY.
RX   MEDLINE=94321350; PubMed=8045907;
RA   McKune K., Woychik N.A.;
RT   "Halobacterial S9 operon contains two genes encoding proteins
RT   homologous to subunits shared by eukaryotic RNA polymerases I, II,
RT   and III.";
RL   J. Bacteriol. 176:4754-4756(1994).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOK / EUKARYOTIC RPB6
CC       RNA POLYMERASE SUBUNIT FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M76567; AAA73100.1; -.
DR   PIR; E41715; E41715.
DR   InterPro; IPR001725; RNA_polK_14KD.
DR   Pfam; PF01192; RNA_pol_K; 1.
DR   PROSITE; PS01111; RNA_POL_K_14KD; 1.
KW   Transferase; DNA-directed RNA polymerase; Transcription.
SQ   SEQUENCE   57 AA;  6291 MW;  D299FDA1954D030F CRC64;


  Query Match             12.4%;  Score 37.5;  DB 1;  Length 57;
  Best Local Similarity   42.9%;  Pred. No. 1.4e+03;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    5;  Gaps    1;

Qy       9 MAPGAVHLPQPVSTRSQHTQP 29
           :| ||     ||   ::||||
Db      21 LAHGA-----PVLIETEHTQP 36


RESULT  11
YPU3_RHOCA
ID   YPU3_RHOCA     STANDARD;      PRT;    55 AA.
AC   P26159;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
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```
DE   Hypothetical 5.8 kDa protein in PUHA 5'region (ORF55).
OS   Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC   Rhodobacter.
OX   NCBI_TaxID=1061;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
RL   Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z11165; CAA77517.1; -.
DR   PIR; S17805; S17805.
KW   Photosynthesis; Hypothetical protein.
SQ   SEQUENCE   55 AA;  5750 MW;  7EB55296266D48B1 CRC64;


  Query Match             12.1%;  Score 36.5;  DB 1;  Length 55;
  Best Local Similarity   40.5%;  Pred. No. 1.6e+03;
  Matches   15;  Conservative    2;  Mismatches   17;  Indels    3;  Gaps    2;

Qy      18 QPVSTRSQHTQPTPEPS--TAPSTSFLLPMGPSP-PA 51
           :| |      || |  |  |||    :  || || ||
Db       9 RPNSAAPARRQPWPCGSCVTAPVAVRIGAMGASPGPA 45


RESULT  12
AP65_CARMA
ID   AP65_CARMA     STANDARD;      PRT;    30 AA.
AC   P82964;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Antibacterial 6.5 kDa protein (Fragment).
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE, AND FUNCTION.
RC   TISSUE=Hemocyte;
RX   MEDLINE=97008941; PubMed=8856051;
RA   Schnapp D., Kemp G.D., Smith V.J.;
RT   "Purification and characterization of a proline-rich antibacterial
RT   peptide, with sequence similarity to bactenecin-7, from the haemocytes
RT   of the shore crab, Carcinus maenas.";
RL   Eur. J. Biochem. 240:532-539(1996).
CC   -!- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST P.IMMOBILIS AND
CC       M.LUTEUS, LESS ACTIVE AGAINST E.COLI D22.
CC   -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW IS: 6.5 kDa.
CC   -!- SIMILARITY: TO BOVINE BACTENECIN 7.
KW   Antibiotic.
FT   NON_TER      30     30
SQ   SEQUENCE   30 AA;  3305 MW;  6E2C2205934896C4 CRC64;


  Query Match             11.9%;  Score 36;  DB 1;  Length 30;
  Best Local Similarity   38.1%;  Pred. No. 1e+03;
  Matches    8;  Conservative    1;  Mismatches    6;  Indels    6;  Gaps    1;

Qy      29 PTPEPSTAPSTSFLLPMGPSP 49
           | | |   |      |:|| |
Db       4 PYPRPFPRP------PIGPRP 18


RESULT  13
ATP8_SQUAC
ID   ATP8_SQUAC     STANDARD;      PRT;    55 AA.
AC   Q9ZZ50;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
GN   MTATP8 OR ATP8.
OS   Squalus acanthias (Spiny dogfish).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
OX   NCBI_TaxID=7797;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99091711; PubMed=9873084;
RA   Rasmussen A.S., Arnason U.;
RT   "Phylogenetic studies of complete mitochondrial DNA molecules place
RT   cartilaginous fishes within the tree of bony fishes.";
RL   J. Mol. Evol. 48:118-123(1999).
CC   -!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC       (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Y18134; CAA77053.1; -.
DR   InterPro; IPR001421; ATP-synt_8.
DR   Pfam; PF00895; ATP-synt_8; 1.
KW   Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT   TRANSMEM      6     26       POTENTIAL.
SQ   SEQUENCE   55 AA;  6587 MW;  3FB9F843CEFA54EE CRC64;


  Query Match             11.9%;  Score 36;  DB 1;  Length 55;
  Best Local Similarity   35.3%;  Pred. No. 1.8e+03;
  Matches   12;  Conservative    2;  Mismatches   12;  Indels    8;  Gaps    1;

Qy      14 VHLPQPVSTRSQHTQPT--------PEPSTAPST 39
           | ||: | |   :  ||        |||   | |
Db      22 VILPKKVMTHLFNNNPTAKSAEKPKPEPWNWPWT 55


RESULT  14
INE1_HUMAN
ID   INE1_HUMAN     STANDARD;      PRT;    51 AA.
AC   O15225;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Putative inactivation escape 1 protein (DXS6974E).
GN   INE1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97386586; PubMed=9244435;
RA   Esposito T., Gianfrancesco F., Ciccodicola A., D'Esposito M.,
RA   Nagaraja R., Mazzarella R., D'Urso M., Forabosco A.;
RT   "Escape from X inactivation of two new genes associated with DXS6974E
RT   and DXS7020E.";
RL   Genomics 43:183-190(1997).
RN   [2]
```

```
RP   REVISIONS.
RA   Forabosco A.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS, HEART AND LIVER
CC       FOLLOWED BY BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
CC       MOSTLY EXPRESSED IN FEMALES.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y10696; CAA71702.2; -.
DR   MIM; 300164; -.
SQ   SEQUENCE   51 AA;  5425 MW;  6F59CC65E58BDBAD CRC64;


  Query Match             11.6%;  Score 35;  DB 1;  Length 51;
  Best Local Similarity   55.6%;  Pred. No. 2e+03;
  Matches   10;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      11 PGAVHLPQPVSTRSQHTQ 28
           || | | | ||  |  ||
Db      27 PGHVALSQTVSPASLLTQ 44


RESULT  15
CA11_RABIT
ID   CA11_RABIT     STANDARD;      PRT;    53 AA.
AC   P02456;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Collagen alpha 1(I) chain (Fragment).
GN   COL1A1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70252720; PubMed=4194291;
RA   Bornstein P., Nesse R.;
RT   "The comparative biochemistry of collagen: the structure of rabbit
RT   skin colllagen and its relevance to immunochemical studies of
RT   collagen.";
RL   Arch. Biochem. Biophys. 138:443-450(1970).
CC   -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
CC       (FIBRILLAR FORMING COLLAGEN).
CC   -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
CC   -!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
CC       BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
CC       HYDROXYAPATITE.
CC   -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
DR   PIR; A02856; CGRB1S.
DR   InterPro; IPR000087; Collagen.
DR   InterPro; IPR001007; VWFC.
DR   PROSITE; PS01208; VWFC; PARTIAL.
KW   Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW   Collagen.
FT   MOD_RES       7      7       CONVERTED TO AN ALDEHYDE GROUP THAT IS
FT                                INVOLVED IN CROSS-LINKING.
FT   MOD_RES      26     26       HYDROXYLATION (PROBABLE).
FT   MOD_RES      29     29       HYDROXYLATION (PROBABLE).
FT   MOD_RES      32     32       HYDROXYLATION (PROBABLE).
FT   MOD_RES      41     41       HYDROXYLATION (PROBABLE).
FT   MOD_RES      44     44       HYDROXYLATION (PROBABLE).
FT   MOD_RES      47     47       HYDROXYLATION (PROBABLE).
FT   NON_TER      53     53
SQ   SEQUENCE   53 AA;  4987 MW;  127582E5E52B87FC CRC64;


  Query Match             11.6%;  Score 35;  DB 1;  Length 53;
  Best Local Similarity   30.2%;  Pred. No. 2.1e+03;
  Matches   13;  Conservative    4;  Mismatches   24;  Indels    2;  Gaps    2;

Qy      14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTG 56
           | :| |:        | |  :  |   |  | | |   ||:|
Db      11 VSVPGPMGPSGPRGLPGPPGAPGPZ-GFZGPPG-ZPGZPGSSG 51


Search completed: August 21, 2002, 10:12:03
Job time: 256 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:07:12 ; Search time 24.13 Seconds
(without alignments)
408.649 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 37469

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60.5	20.0	52	4	Q14441	Q14441 homo sapien
2	55.5	18.4	42	4	Q16469	Q16469 homo sapien
3	52	17.2	52	12	O92313	O92313 human respi
4	51	16.9	52	12	O92301	O92301 human respi
5	51	16.9	52	12	O92314	O92314 human respi
6	50.5	16.7	33	6	O02832	O02832 gorilla gor
7	50.5	16.7	54	11	Q9WTY7	Q9wty7 mus musculu
8	50	16.6	52	6	Q9GL38	Q9gl38 bos taurus
9	49.5	16.4	54	12	Q9J7C8	Q9j7c8 simian viru
10	49	16.2	46	4	Q15218	Q15218 homo sapien
11	49	16.2	51	6	O18723	O18723 macaca fusc
12	49	16.2	52	12	O92302	O92302 human respi
13	49	16.2	52	12	O92303	O92303 human respi
14	48	15.9	38	4	Q9HB17	Q9hb17 homo sapien
15	48	15.9	42	6	Q9GKJ3	Q9gkj3 sus scrofa
16	47.5	15.7	27	10	Q9S8M0	Q9s8m0 solanum tub
17	47.5	15.7	44	5	Q95XP8	Q95xp8 caenorhabdi
18	47.5	15.7	57	4	Q13697	Q13697 homo sapien
19	47.5	15.7	57	5	Q9VQU6	Q9vqu6 drosophila
20	47	15.6	31	2	Q9Z516	Q9z516 streptomyce
21	47	15.6	52	12	O92300	O92300 human respi
22	47	15.6	52	12	O92311	O92311 human respi
23	46	15.2	40	4	Q14069	Q14069 homo sapien
24	46	15.2	55	8	O79966	O79966 mogurnda ad
25	46	15.2	55	8	O79998	O79998 mogurnda ad
26	45.5	15.1	20	10	Q41179	Q41179 chlamydomon
27	45.5	15.1	52	15	Q993P6	Q993p6 human immun
28	45.5	15.1	54	4	Q9H3T0	Q9h3t0 homo sapien
29	45	14.9	50	12	Q9JFE6	Q9jfe6 vaccinia vi
30	45	14.9	51	12	Q9WL72	Q9wl72 human respi
31	45	14.9	52	12	O92309	O92309 human respi
32	45	14.9	52	12	O92310	O92310 human respi
33	45	14.9	52	12	Q9WL69	Q9wl69 human respi
34	45	14.9	52	12	O92319	O92319 human respi
35	45	14.9	53	12	Q65541	Q65541 bovine herp
36	44.5	14.7	44	12	Q9WA44	Q9wa44 human respi
37	44.5	14.7	44	12	O92307	O92307 human respi
38	44.5	14.7	53	4	Q9BUX7	Q9bux7 homo sapien
39	44.5	14.7	55	5	O61039	O61039 trypanosoma
40	44.5	14.7	57	10	Q94JS2	Q94js2 arabidopsis
41	44	14.6	28	7	Q31629	Q31629 homo sapien
42	44	14.6	49	6	Q9MYS0	Q9mys0 oryctolagus
43	44	14.6	56	6	Q29163	Q29163 sus scrofa
44	43.5	14.4	44	12	O92317	O92317 human respi
45	43.5	14.4	50	6	Q29321	Q29321 sus scrofa

ALIGNMENTS

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RESULT   1
Q14441
ID   Q14441      PRELIMINARY;      PRT;    52 AA.
AC   Q14441;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   GLYCOPROTEIN IB ALPHA (FRAGMENT).
GN   GPIB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ishida F.;
RT   "Submission.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L39103; AAA69491.1; -.
DR   InterPro; IPR002965; P_rich_extensn.
DR   PRINTS; PR01217; PRICHEXTENSN.
FT   NON_TER       1      1
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  5187 MW;  829FBEB4792EA30F CRC64;


  Query Match             20.0%;  Score 60.5;  DB 4;  Length 52;
  Best Local Similarity   34.7%;  Pred. No. 7.6;
  Matches   17;  Conservative    7;  Mismatches   20;  Indels    5;  Gaps    3;

Qy       1 TSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           |:  ||   ||      |:| |  :  :  ||||:: |: |   |  | |
Db       8 TTPEPTSEPAPSPT-TPEPTSEPAP-SPTTPEPTSEPAPS---PTTPEP 51


RESULT   2
Q16469
ID   Q16469      PRELIMINARY;      PRT;    42 AA.
AC   Q16469;
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DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   GLYCOPROTEIN IB ALPHA VARIANT B (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92250564; PubMed=1577776;
RA   Lopez J.A., Ludwig E.H., McCarthy B.J.;
RT   "Polymorphism of human glycoprotein Ib alpha results from a variable
RT   number of tandem repeats of a 13-amino acid sequence in the mucin-like
RT   macroglycopeptide region. Structure/function implications.";
RL   J. Biol. Chem. 267:10055-10061(1992).
DR   EMBL; S34439; AAB22153.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   42 AA;  4222 MW;  228018AC7FBE3F38 CRC64;


  Query Match             18.4%;  Score 55.5;  DB 4;  Length 42;
  Best Local Similarity   35.6%;  Pred. No. 21;
  Matches   16;  Conservative    6;  Mismatches   18;  Indels    5;  Gaps    3;

Qy       5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           ||   ||     |:| |  :  :  ||||:: |: |   |  | |
Db       2 PTSEPAPSPT-TPEPTSEPAP-SPTTPEPTSEPAPS---PTTPEP 41


RESULT   3
O92313
ID   O92313      PRELIMINARY;      PRT;    52 AA.
AC   O92313;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS   Human respiratory syncytial virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11250;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=196775;
RX   MEDLINE=99036758; PubMed=9817872;
RA   Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT   "Genetic variability among group A and group B respiratory syncytial
RT   viruses in a children's hospital.";
RL   J. Clin. Microbiol. 36:3552-3557(1998).
DR   EMBL; AF086886; AAC43006.1; -.
DR   InterPro; IPR000925; Glycoprot_G.
DR   Pfam; PF00802; Glycoprotein_G; 1.
FT   NON_TER       1      1
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  5541 MW;  8C3111FE05DF29E0 CRC64;


  Query Match             17.2%;  Score 52;  DB 12;  Length 52;
  Best Local Similarity   34.3%;  Pred. No. 63;
  Matches   12;  Conservative    4;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      15 HLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           |  |   :  |  ::  | ||   :||  |   |||
Db      13 HTSQKETLHSTSSEGNPSPSQVYTTSEYLSQSPSP 47


RESULT   4
O92301
ID   O92301      PRELIMINARY;      PRT;    52 AA.
AC   O92301;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS   Human respiratory syncytial virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11250;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=181691;
RX   MEDLINE=99036758; PubMed=9817872;
RA   Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT   "Genetic variability among group A and group B respiratory syncytial
RT   viruses in a children's hospital.";
RL   J. Clin. Microbiol. 36:3552-3557(1998).
DR   EMBL; AF086872; AAC42992.1; -.
DR   InterPro; IPR000925; Glycoprot_G.
DR   Pfam; PF00802; Glycoprotein_G; 1.
FT   NON_TER       1      1
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  5613 MW;  7C3114ACA02574E6 CRC64;


  Query Match             16.9%;  Score 51;  DB 12;  Length 52;
  Best Local Similarity   34.3%;  Pred. No. 81;
  Matches   12;  Conservative    4;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      15 HLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           |  |   :  |  ::  | ||   :||  |   |||
Db      13 HTSQKETLHSTTSEGNPSPSQVYTTSEYLSQSPSP 47


RESULT   5
O92314
ID   O92314      PRELIMINARY;      PRT;    52 AA.
AC   O92314;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS   Human respiratory syncytial virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11250;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=203721;
RX   MEDLINE=99036758; PubMed=9817872;
RA   Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT   "Genetic variability among group A and group B respiratory syncytial
RT   viruses in a children's hospital.";
RL   J. Clin. Microbiol. 36:3552-3557(1998).
DR   EMBL; AF086888; AAC43008.1; -.
DR   InterPro; IPR000925; Glycoprot_G.
DR   Pfam; PF00802; Glycoprotein_G; 1.
FT   NON_TER       1      1
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  5554 MW;  3B328FBC5B4E9858 CRC64;


  Query Match             16.9%;  Score 51;  DB 12;  Length 52;
  Best Local Similarity   31.8%;  Pred. No. 81;
  Matches   14;  Conservative    5;  Mismatches   25;  Indels    0;  Gaps    0;

Qy       6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
           | |:     |  |  :  |  ::    || | :||  |   |||
Db       4 TNSITGNLEHTSQEETLHSTSSEGNTSPSQAYTTSEYLSQPPSP 47


RESULT   6
O02832
ID   O02832      PRELIMINARY;      PRT;    33 AA.
AC   O02832;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
```

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DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HUNTINGTIN PROTEIN (FRAGMENT).
GN   IT15.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96326790; PubMed=8766138;
RA   Pecheux C., Gall A.L., Kaplan J.C., Dode C.;
RT   "Sequence analysis of the CAG triplet repeats region in the Huntington
RT   disease gene (IT15) in several mammalian species.";
RL   Ann. Genet. 39:81-86(1996).
DR   EMBL; S83377; AAB50771.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   33 AA;  3393 MW;  44F558CE5636722A CRC64;


  Query Match             16.7%;  Score 50.5;  DB 6;  Length 33;
  Best Local Similarity   38.5%;  Pred. No. 58;
  Matches   15;  Conservative    1;  Mismatches   12;  Indels   11;  Gaps    3;

Qy      16 LPQPVSTRSQHTQP-TPEPSTAPSTSFLLPMGPSPPAEG 53
           ||||      | ||  |:|   |      |  | ||  |
Db       2 LPQP----PPHGQPLLPQPQPQP------PPPPPPPPG 30


RESULT   7
Q9WTY7
ID   Q9WTY7      PRELIMINARY;      PRT;    54 AA.
AC   Q9WTY7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   ENDOTHELIAL NITRIC OXIDE SYNTHASE (FRAGMENT).
GN   NOS3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV129;
RX   MEDLINE=99096466; PubMed=9878824;
RA   Teichert A.M., Karantzoulis-Fegaras F., Wang Y., Mawji I.A., Bei X.,
RA   Gnanapandithen K., Marsden P.A.;
RT   "Characterization of the murine endothelial nitric oxide synthase
RT   promoter.";
RL   Biochim. Biophys. Acta 1443:352-357(1998).
DR   EMBL; AF091262; AAD22613.1; -.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  5193 MW;  1DA456A21958B2EA CRC64;


  Query Match             16.7%;  Score 50.5;  DB 11;  Length 54;
  Best Local Similarity   47.8%;  Pred. No. 95;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    5;  Gaps    1;

Qy      29 PTPEPSTAPSTSFLLPMGPSPPA 51
           | ||||  ||:      |  |: ||
Db      34 PAPEPSQAPA-----PPSPTRPA 51


RESULT   8
Q9GL38
ID   Q9GL38      PRELIMINARY;      PRT;    52 AA.
AC   Q9GL38;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   CALPASTATIN (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chung H.Y., Davis M.E., Hines H.C.;
RT   "PCR-SSCP analysis of the bovine calpastatin gene domain L region.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY008267; AAG23869.1; -.
FT   NON_TER       1      1
FT   NON_TER      52     52
SQ   SEQUENCE   52 AA;  5749 MW;  CBD5A7449AFDDA89 CRC64;


  Query Match             16.6%;  Score 50;  DB 6;  Length 52;
  Best Local Similarity   33.3%;  Pred. No. 1e+02;
  Matches   11;  Conservative    3;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAP 37
           |  |   |: | |:  :       ||  | || |
Db      19 PKHSSDTGSKHAPKEKAVSKSSEQPPSEKSTKP 51


RESULT   9
Q9J7C8
ID   Q9J7C8      PRELIMINARY;      PRT;    54 AA.
AC   Q9J7C8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LARGE T ANTIGEN (FRAGMENT).
OS   Simian virus 40 (SV40).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10633;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MC-028863B-1;
RX   MEDLINE=20090224; PubMed=10626798;
RA   Rizzo P., Di Resta I., Powers A., Ratner H., Carbone M.;
RT   "Unique strains of SV40 in commercial poliovaccines from 1955 not
RT   readily identifiable with current testing for SV40 infection.";
RL   Cancer Res. 59:6103-6108(1999).
DR   EMBL; AF180738; AAF28272.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   54 AA;  5868 MW;  556CDAB682C1EFCD CRC64;


  Query Match             16.4%;  Score 49.5;  DB 12;  Length 54;
  Best Local Similarity   32.7%;  Pred. No. 1.2e+02;
  Matches   16;  Conservative    5;  Mismatches   25;  Indels    3;  Gaps    2;

Qy       8 SMAPGAVHLPQP-VSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 55
           | : |:   |||  |::| |    |       |    |  |:|| |  |
Db       8 SQSQGSFQAPQPSQSSQSXHDHNQPYHICRGXTCXKKP--PTPPPEPET 54


RESULT  10
Q15218
ID   Q15218      PRELIMINARY;      PRT;    46 AA.
AC   Q15218;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   SALIVARY PROLINE-RICH PROTEIN 2 (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84298176; PubMed=6089212;
```

```
RA   Azen E.A., Lyons K.M., McGonigal T., Barrett N.L., Clements L.S.,
RA   Maeda N., Vanin E.F., Carlson D.M., Smithies O.;
RT   "Clones from the human gene complex coding for salivary proline-rich
RT   proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:5561-5565(1984).
DR   EMBL; K02578; AAA36505.1; -.
FT   NON_TER       1       1
FT   NON_TER      46      46
SQ   SEQUENCE   46 AA;  4592 MW;  FCE1D38D8DEDC173 CRC64;


  Query Match             16.2%;  Score 49;  DB 4;  Length 46;
  Best Local Similarity   38.2%;  Pred. No. 1.2e+02;
  Matches   13;  Conservative    2;  Mismatches   15;  Indels    4;  Gaps    1;

Qy      21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS 54
           | ||    |  :|   |      | || ||| |:
Db       1 SARS----PPRKPQGPPQQEGNNPQGPPPPAGGN 30


RESULT  11
O18723
ID   O18723      PRELIMINARY;      PRT;    51 AA.
AC   O18723;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
GN   DAF.
OS   Macaca fuscata fuscata (Japanese macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9543;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=98099759; PubMed=9435343;
RA   Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;
RT   "A new repetitive sequence uniquely present in the decay-accelerating
RT   factor genes.";
RL   Immunogenetics 47:246-255(1998).
CC   -!- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC       (RCA) FAMILY.
DR   EMBL; AB003315; BAA22903.1; -.
KW   Complement pathway.
FT   NON_TER       1       1
FT   NON_TER      51      51
SQ   SEQUENCE   51 AA;  5545 MW;  ED112B05C37548A6 CRC64;


  Query Match             16.2%;  Score 49;  DB 6;  Length 51;
  Best Local Similarity   28.9%;  Pred. No. 1.3e+02;
  Matches   13;  Conservative    6;  Mismatches   22;  Indels    4;  Gaps    1;

Qy      11 PGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGST 55
           |  |   |  |: |:    || : :| |:         | ||  :|
Db       3 PPTVQKPTTVNVRTTEVSPTSQKTTTPNAQ----ATRSTPASRTT 43


RESULT  12
O92302
ID   O92302      PRELIMINARY;      PRT;    52 AA.
AC   O92302;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS   Human respiratory syncytial virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11250;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=182473;
RX   MEDLINE=99036758; PubMed=9817872;
RA   Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT   "Genetic variability among group A and group B respiratory syncytial
RT   viruses in a children's hospital.";
RL   J. Clin. Microbiol. 36:3552-3557(1998).
DR   EMBL; AF086873; AAC42993.1; -.
DR   InterPro; IPR000925; Glycoprot_G.
DR   Pfam; PF00802; Glycoprotein_G; 1.
FT   NON_TER       1       1
FT   NON_TER      52      52
SQ   SEQUENCE   52 AA;  5530 MW;  C2029E4C5B551270 CRC64;


  Query Match             16.2%;  Score 49;  DB 12;  Length 52;
  Best Local Similarity   31.8%;  Pred. No. 1.3e+02;
  Matches   14;  Conservative    4;  Mismatches   26;  Indels    0;  Gaps    0;

Qy      6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
          | |      |  |  :  |  ::    || | :||  |   |||
Db      4 TNSTTGNLEHTSQEETLHSTSSEGNTSPSQAYTTSEYLSQPPSP 47


RESULT  13
O92303
ID   O92303      PRELIMINARY;      PRT;    52 AA.
AC   O92303;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS   Human respiratory syncytial virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX   NCBI_TaxID=11250;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=182701;
RX   MEDLINE=99036758; PubMed=9817872;
RA   Coggins W.B., Lefkowitz E.J., Sullender W.M.;
RT   "Genetic variability among group A and group B respiratory syncytial
RT   viruses in a children's hospital.";
RL   J. Clin. Microbiol. 36:3552-3557(1998).
DR   EMBL; AF086874; AAC42994.1; -.
DR   InterPro; IPR000925; Glycoprot_G.
DR   Pfam; PF00802; Glycoprotein_G; 1.
FT   NON_TER       1       1
FT   NON_TER      52      52
SQ   SEQUENCE   52 AA;  5542 MW;  C2028FBC5B551270 CRC64;


  Query Match             16.2%;  Score 49;  DB 12;  Length 52;
  Best Local Similarity   31.8%;  Pred. No. 1.3e+02;
  Matches   14;  Conservative    4;  Mismatches   26;  Indels    0;  Gaps    0;

Qy      6 TRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSP 49
          | |      |  |  :  |  ::    || | :||  |   |||
Db      4 TNSTTGNLEHTSQEETLHSTSSEGNTSPSQAYTTSEYLSQPPSP 47


RESULT  14
Q9HB17
ID   Q9HB17      PRELIMINARY;      PRT;    38 AA.
AC   Q9HB17;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIGNALING MOLECULE SPEC1 BETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pirone D.M., Fukihara S., Gutkind S.J., Burbelo P.D.;
RT   "SPECs, small binding proteins for CDC42 proteins.";
RL   J. Biol. Chem. 0:0-0(2000).
DR   EMBL; AF286592; AAG17723.1; -.
DR   InterPro; IPR001230; Prenyltn.
DR   PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ   SEQUENCE   38 AA;  4245 MW;  3B416F3C5ADF4E91 CRC64;


  Query Match             15.9%;  Score 48;  DB 4;  Length 38;
  Best Local Similarity   46.7%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    2;  Mismatches    6;  Indels    8;  Gaps    2;

Qy      14 VHLPQPVSTRSQHTQPTPEPSTAPSTSFLL 43
           |  |||||        ||| |:  | :| ||
Db      13 VEKPQPVSL------PTPHPN--PKSSQLL 34


RESULT  15
Q9GKJ3
ID   Q9GKJ3      PRELIMINARY;      PRT;    42 AA.
AC   Q9GKJ3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
GN   MYLK.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Van Poucke M., Yerle M., Tuggle C., Chardon P., Van Zeveren A.,
RA   Peelman L.J.;
RT   "Integration of porcine chromosome 13 maps.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF222917; AAG41130.1; -.
KW   Kinase.
FT   NON_TER       1      1
FT   NON_TER      42     42
SQ   SEQUENCE   42 AA;  4677 MW;  78BDD867E66EF64F CRC64;


  Query Match             15.9%;  Score 48;  DB 6;  Length 42;
  Best Local Similarity   36.6%;  Pred. No. 1.4e+02;
  Matches   15;  Conservative    2;  Mismatches   14;  Indels   10;  Gaps    2;

Qy      14 VHLPQPVSTRS----QHTQPTPEPSTAPSTSFLLPMGPSPP 50
           || || |  ||     : |  || |   |      |  |: |
Db       8 VHSPQQVDFRSVLAKKGTPKTPVPEKLP------PPKPTTP 42


Search completed: August 21, 2002, 10:11:47
Job time: 275 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:03:27 ; Search time 29.62 Seconds
(without alignments)
213.748 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 375566

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81.5	27.0	51	22	ABG08614	Novel human diagno
2	68.5	22.7	47	21	AAB56300	Human secreted pro
3	67.5	22.4	49	19	AAW59911	Amino acid sequenc
4	66.5	22.0	52	22	AAU42052	Propionibacterium
5	63.5	21.0	55	22	AAU44730	Propionibacterium
6	61	20.2	47	22	AAO07479	Human polypeptide
7	60	19.9	57	22	AAU64419	Propionibacterium
8	59	19.5	45	12	AAR15261	Linking B region #
9	58	19.2	52	22	AAU63462	Propionibacterium
10	58	19.2	54	15	AAR49722	Sequence of a pept
11	58	19.2	54	15	AAR49536	Camel Ig 2-heavy c
12	57	18.9	53	22	ABG14378	Novel human diagno
13	56.5	18.7	41	20	AAY01285	Peptide encoded by
14	56.5	18.7	56	22	AAO06362	Human polypeptide
15	56	18.5	47	22	ABB38671	Peptide #6177 enco
16	56	18.5	47	22	ABB23747	Protein #5746 enco
17	56	18.5	47	22	AAM59300	Human brain expres
18	56	18.5	47	22	AAM71847	Human bone marrow
19	56	18.5	47	22	AAM19336	Peptide #5770 enco
20	56	18.5	47	22	AAM32132	Peptide #6169 enco
21	56	18.5	50	22	AAM80671	Human haematologic
22	56	18.5	53	22	AAU52934	Propionibacterium
23	55.5	18.4	39	22	AAO07489	Human polypeptide
24	55	18.2	46	20	AAW88522	Amphotropic hyperv
25	55	18.2	51	22	AAU50103	Propionibacterium
26	55	18.2	52	22	AAB61193	Human INTERCEPT 21
27	55	18.2	56	22	ABG12636	Novel human diagno
28	54.5	18.0	53	22	AAU43161	Propionibacterium
29	54.5	18.0	55	21	AAB42690	Human ORFX ORF2454
30	54	17.9	21	9	AAP81606	Sequence of human
31	54	17.9	36	21	AAY65289	Human 5' EST relat
32	54	17.9	50	22	ABB31801	Peptide #4452 enco
33	54	17.9	50	22	ABB37029	Peptide #4535 enco
34	54	17.9	50	22	ABB22345	Protein #4344 enco
35	54	17.9	50	22	AAM57757	Human brain expres
36	54	17.9	50	22	AAM70172	Human bone marrow
37	54	17.9	50	22	AAM17997	Peptide #4431 enco
38	54	17.9	50	22	AAM30506	Peptide #4543 enco
39	54	17.9	50	22	AAM05637	Peptide #4319 enco
40	53.5	17.7	32	22	AAO08605	Human polypeptide
41	53.5	17.7	37	18	AAW26641	H. insolens family
42	53.5	17.7	57	22	AAU63823	Propionibacterium
43	53	17.5	30	22	AAO02051	Human polypeptide
44	53	17.5	52	22	AAU40874	Propionibacterium
45	53	17.5	57	22	AAU51526	Propionibacterium

ALIGNMENTS

RESULT 1
ABG08614
ID ABG08614 standard; Protein; 51 AA.
XX
AC ABG08614;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #8605.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS72801.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess

PT biodiversity -
XX
PS Claim 20; SEQ ID No 38973; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 51 AA;

Query Match 27.0%; Score 81.5; DB 22; Length 51;
Best Local Similarity 41.7%; Pred. No. 0.27;
Matches 20; Conservative 5; Mismatches 18; Indels 5; Gaps 1;

```
Qy      3 TSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
          | || | :|  | : || |:      | | ||: |     ||: ||||
Db      2 tfptfsssphlvmmiqpsssspppplpppppsspp-----lplppspp 44
```

RESULT 2
AAB56300
ID AAB56300 standard; Protein; 47 AA.
XX
AC AAB56300;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 99 SEQ ID NO:394.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; pathological condition;
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; skin aging; food additive; preservative.
XX
OS Homo sapiens.
XX
PN WO200070042-A1.
XX
PD 23-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12788.
XX
PR 13-MAY-1999; 99US-0134068.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
PI Duan RD, Florence KA, Soppet DR;
XX

DR WPI; 2000-679828/66.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; Page 1035; 1065pp; English.
XX
CC The polynucleotide sequences given in AAC99818 to AAC99977 encode the
CC human secreted proteins given in AAB56077 to AAB56362. Human secreted
CC proteins have activities based on the tissues and cells the genes are
CC expressed in. Examples of activities include: immunosuppressive;
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
CC virucide; fungicide; and opthalmalogical. The human secreted
CC polynucleotides and proteins can be used to prevent, treat or ameliorate
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. They are also used in diagnosing a pathological
CC condition or susceptibility to a pathological condition. Disorders which
CC are diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The proteins can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The proteins can also be used as a
CC food additive or preservative to increase or decrease storage
CC capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 47 AA;

Query Match 22.7%; Score 68.5; DB 21; Length 47;
Best Local Similarity 40.5%; Pred. No. 4.7;
Matches 17; Conservative 3; Mismatches 17; Indels 5; Gaps 1;

```
Qy     19 PVSTRSQHTQPTPE-----PSTAPSTSFLLPMGPSPPAEGST 55
          ||||      |||      |: :| |    |  |||||  |:
Db      5 pvstlplgpsptpshtahpptpspptpxshpsxpsppatsss 46
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RESULT 3
AAW59911
ID AAW59911 standard; peptide; 49 AA.
XX
AC AAW59911;
XX
DT 20-NOV-1998 (first entry)
XX
DE Amino acid sequence of the mutanase enzyme PT box.
XX
KW Mutanase enzyme; PT box; alpha-1,3 glucoside bond; mutan; plaque;
KW bacteria; teeth.
XX
OS Bacillus sp.
XX
PN JP10201483-A.
XX
PD 04-AUG-1998.
XX
PF 01-OCT-1997; 97JP-0284362.
XX
PR 25-NOV-1996; 96JP-0314057.
XX
PA (LIOY) LION CORP.
XX
DR WPI; 1998-474495/41.
XX
PT Gene encoding a mutanase enzyme - used for prevention and removal
PT of plaque and bacteria on teeth

XX
PS Claim 2; Page 5; 15pp; Japanese.
XX
CC This is the amino acid sequence of the mutanase enzyme PT box, which
CC decomposes the alpha-1,3 glucoside bond of mutan. The mutanase enzyme
CC is used in the method of the invention for prevention and removal of
CC plaque and bacteria on teeth.
XX
SQ Sequence 49 AA;

Query Match 22.4%; Score 67.5; DB 19; Length 49;
Best Local Similarity 35.3%; Pred. No. 6.1;
Matches 18; Conservative 6; Mismatches 22; Indels 5; Gaps 2;

Qy 1 TST-SPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
Db 2 tstptptpsptptptptptptptptptptptptptptptptpt----ptptpp 48

RESULT 4
AAU42052
ID AAU42052 standard; Protein; 52 AA.
XX
AC AAU42052;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #2948.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59516.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 3247; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 52 AA;

Query Match 22.0%; Score 66.5; DB 22; Length 52;
Best Local Similarity 35.6%; Pred. No. 8.1;
Matches 16; Conservative 5; Mismatches 21; Indels 3; Gaps 1;

Qy 10 APGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGS 54
Db 1 apgtpgnpraratrgeptdpvvrp---pekataiptfppppaans 42

RESULT 5
AAU44730
ID AAU44730 standard; Protein; 55 AA.
XX
AC AAU44730;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #5626.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59524.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 5925; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The

```
CC   polypeptides may be used as antigens in the production of antibodies
CC   specific for P. acnes proteins. These antibodies can be used to
CC   downregulate expression and activity of P. acnes polypeptides and
CC   therefore treat P. acnes infections. The antibodies may also be used as
CC   diagnostic agents for determining P. acnes presence, for example, by
CC   enzyme linked immunosorbent assay (ELISA).
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   55 AA;


  Query Match             21.0%;  Score 63.5;  DB 22;  Length 55;
  Best Local Similarity   40.0%;  Pred. No. 17;
  Matches   16;  Conservative    3;  Mismatches   18;  Indels    3;  Gaps    1;

Qy       8 SMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGP 47
           |  ||    || | |: :|: |   | | || |     ||
Db       3 srtpgk---pqtvrtkkrhsgpidapetrpspsapqicgp 39


RESULT   6
AAO07479
ID   AAO07479 standard; Protein; 47 AA.
XX
AC   AAO07479;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 21371.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI87410.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 21371; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   47 AA;


  Query Match             20.2%;  Score 61;  DB 22;  Length 47;
  Best Local Similarity   38.6%;  Pred. No. 25;
  Matches   17;  Conservative    5;  Mismatches   16;  Indels    6;  Gaps    2;

Qy       5 PTRSMAPGAVHLPQPVSTRSQHTQPTPE-PSTAPSTSFLLPMGP 47
           |||    |   | |      :||:|||  |:    |: |||: |
Db       3 ptrprtrgvkilxq-----fehtkptpglptlialttlllpisp 41


RESULT   7
AAU64419
ID   AAU64419 standard; Protein; 57 AA.
XX
AC   AAU64419;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Propionibacterium acnes immunogenic protein #25315.
XX
KW   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW   uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW   inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW   dermatological; osteopathic; neuroprotectant.
XX
OS   Propionibacterium acnes.
XX
PN   WO200181581-A2.
XX
PD   01-NOV-2001.
XX
PF   20-APR-2001; 2001WO-US12865.
XX
PR   21-APR-2000; 2000US-199047P.
PR   02-JUN-2000; 2000US-208841P.
PR   07-JUL-2000; 2000US-216747P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Skeiky YAW,  Persing DH,  Mitcham JL,  Wang SS,  Bhatia A;
PI   L'maisonneuve J,  Zhang Y,  Jen S,  Carter D;
XX
DR   WPI; 2001-616774/71.
DR   N-PSDB; AAS59643.
XX
PT   Propionibacterium acnes polypeptides and nucleic acids useful for
PT   vaccinating against and diagnosing infections, especially useful for
PT   treating acne vulgaris -
XX
PS   Example 1; SEQ ID No 25614; 1069pp; English.
XX
CC   Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC   polypeptides. The proteins and their associated DNA sequences are used in
CC   the treatment, prevention and diagnosis of medical conditions caused by
CC   P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC   pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC   P. acnes is also involved in infections of bone, joints and the central
CC   nervous system, however it is particularly involved in the inflammatory
CC   lesions associated with acne vulgaris. A method for detecting the
CC   presence or absence of P. acnes in a patient comprises contacting a
CC   sample with a binding agent that binds to the proteins of the invention
CC   and determining the amount of bound protein in the sample. The
CC   polypeptides may be used as antigens in the production of antibodies
CC   specific for P. acnes proteins. These antibodies can be used to
CC   downregulate expression and activity of P. acnes polypeptides and
CC   therefore treat P. acnes infections. The antibodies may also be used as
CC   diagnostic agents for determining P. acnes presence, for example, by
CC   enzyme linked immunosorbent assay (ELISA).
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CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   57 AA;


  Query Match             19.9%;  Score 60;  DB 22;  Length 57;
  Best Local Similarity   43.6%;  Pred. No. 39;
  Matches   17;  Conservative    2;  Mismatches   10;  Indels   10;  Gaps    2;

Qy      2 STSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTS 40
          |||| |: ||   | | |  | :|       ||  | ||
Db      7 stspgrtsap---hepspavtgnq-------psrrpkts 35


RESULT   8
AAR15261
ID   AAR15261 standard; Protein; 45 AA.
XX
AC   AAR15261;
XX
DT   12-FEB-1992  (first entry)
XX
DE   Linking B region #8 derived from a (hemi)cellulose-degrading enzyme.
XX
KW   CBD; hemicellulosic substrate;
KW   Trichoderma reesei; cellulase; terminal A region.
XX
PN   WO9117244-A.
XX
PD   14-NOV-1991.
XX
PF   08-MAY-1991;   91WO-DK00124.
XX
PR   09-MAY-1990;   90DK-0001158.
XX
PA   (NOVO ) NOVO NORDISK A/S.
XX
PI   Woldike HF,  Hagen F,  Hjort CM,  Hastrup S;
XX
DR   WPI; 1991-353766/48.
XX
PT   New fungal (hemi)cellulose degrading enzymes - for prodn. of liq.
PT   fuel gas and feed protein, have specified carbohydrate binding domain
XX
PS   Claim 23; Page 46; 73pp; English.
XX
CC   This is one of 8 specified linking B regions which are derived from
CC   a cellulose- or hemicellulose-degrading enzyme and which are
CC   enriched in the amino acids Gly and/or Asn and/or Pro and/or Ser
CC   and/or Thr and/or Gln. It can be incorporated in a fusion
CC   protein comprising a catalytic domain from a cellulase, e.g. a
CC   Bacillus endoglucanase, and a carbohydrate binding domain from a
CC   a fungal endoglucanase. See also AAR15254-R15260.
XX
SQ   Sequence   45 AA;


  Query Match             19.5%;  Score 59;  DB 12;  Length 45;
  Best Local Similarity   37.8%;  Pred. No. 38;
  Matches   17;  Conservative    8;  Mismatches   18;  Indels    2;  Gaps    2;

Qy     13 AVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEGSTGD 57
          || :|   || |   |||   :|: ||:   |: |: |: | | :
Db      2 avqipss-stsspvnqptststtststtssppvqpttps-gctae 44


RESULT   9
AAU63462
ID   AAU63462 standard; Protein; 52 AA.
XX
AC   AAU63462;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Propionibacterium acnes immunogenic protein #24358.
XX
KW   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW   uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW   inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW   dermatological; osteopathic; neuroprotectant.
XX
OS   Propionibacterium acnes.
XX
PN   WO200181581-A2.
XX
PD   01-NOV-2001.
XX
PF   20-APR-2001; 2001WO-US12865.
XX
PR   21-APR-2000; 2000US-199047P.
PR   02-JUN-2000; 2000US-208841P.
PR   07-JUL-2000; 2000US-216747P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Skeiky YAW,  Persing DH,  Mitcham JL,  Wang SS,  Bhatia A;
PI   L'maisonneuve J,  Zhang Y,  Jen S,  Carter D;
XX
DR   WPI; 2001-616774/71.
DR   N-PSDB; AAS59633.
XX
PT   Propionibacterium acnes polypeptides and nucleic acids useful for
PT   vaccinating against and diagnosing infections, especially useful for
PT   treating acne vulgaris -
XX
PS   Example 1; SEQ ID No 24657; 1069pp; English.
XX
CC   Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC   polypeptides. The proteins and their associated DNA sequences are used in
CC   the treatment, prevention and diagnosis of medical conditions caused by
CC   P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC   pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC   P. acnes is also involved in infections of bone, joints and the central
CC   nervous system, however it is particularly involved in the inflammatory
CC   lesions associated with acne vulgaris. A method for detecting the
CC   presence or absence of P. acnes in a patient comprises contacting a
CC   sample with a binding agent that binds to the proteins of the invention
CC   and determining the amount of bound protein in the sample. The
CC   polypeptides may be used as antigens in the production of antibodies
CC   specific for P. acnes proteins. These antibodies can be used to
CC   downregulate expression and activity of P. acnes polypeptides and
CC   therefore treat P. acnes infections. The antibodies may also be used as
CC   diagnostic agents for determining P. acnes presence, for example, by
CC   enzyme linked immunosorbent assay (ELISA).
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   52 AA;


  Query Match             19.2%;  Score 58;  DB 22;  Length 52;
  Best Local Similarity   36.6%;  Pred. No. 55;
  Matches   15;  Conservative    5;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPM 45
          |||:  |  : || | |  |   :  |  ||: | |   |:
Db     12 ptrtypparlrlpspssrcsilqrrypsrststsvsartpv 52


RESULT  10
AAR49722
ID   AAR49722 standard; peptide; 54 AA.
XX
```

```
AC   AAR49722;
XX
DT   22-AUG-1994  (first entry)
XX
DE   Sequence of a peptide which is part of the heavy (H) chain (CH3) of an
DE   immunoglobulin (Ig).
XX
KW   Immunoglobulin; heavy chain; Camelid.
XX
OS   Camelus dromedarius.
XX
PN   WO9404678-A.
XX
PD   03-MAR-1994.
XX
PF   18-AUG-1993;   93WO-EP02214.
XX
PR   21-AUG-1992;   92EP-0402326.
PR   21-MAY-1993;   93EP-0401310.
XX
PA   (CAST/) CASTERMAN C.
PA   (HAME/) HAMERS R.
XX
PI   Casterman C,  Hamers R;
XX
DR   WPI; 1994-083195/10.
XX
PT   Immunoglobulins devoid of light chains - also processes for their
PT   preparation, and protein and nucleotide sequence encoding them.
XX
PS   Claim 21; Page 65; 87pp; English.
XX
CC   A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)
CC   polypeptide chains sufficient for the formation of a complete
CC   antigen binding site or several such chains. The Ig is devoid of
CC   light (L) polypeptide chains. The Ig may be obtd. from prokaryotic
CC   cells, esp. E. coli, by: cloning a DNA or cDNA sequence coding for
CC   the VH domain of an Ig devoid of L chains obtainable from e.g.
CC   lymphocytes of Camelids; recovering the cloned fragment after
CC   amplification using a 5' primer contg. an Xho site and a 3' primer
CC   contg. the Spe site having the sequence in AAQ44383; cloning the
CC   recovered fragment is a vector; transforming host cells; and
CC   recovering the expression product of the VHH coding sequence.
CC   A nucleotide encoding the peptides in AAR49721-24 is claimed.
XX
SQ   Sequence   54 AA;


  Query Match             19.2%;  Score 58;  DB 15;  Length 54;
  Best Local Similarity   31.6%;  Pred. No. 57;
  Matches   12;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy     16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
          :|||        || |:|   |      |  |:|   |
Db      9 ipqpqpkpqpqpqpqpkpqpkpepectcpkcpapellg 46


RESULT  11
AAR49536
ID   AAR49536 standard; peptide; 54 AA.
XX
AC   AAR49536;
XX
DT   04-SEP-1994  (first entry)
XX
DE   Camel Ig 2-heavy chain molecule (clone no. 72/79).
XX
KW   Immunoglobulin; Ig; heavy chain; constant region; variable region;
KW   antibody engineering; IgG2; IgG3.
XX
OS   Camelus dromadarius.
XX
FH   Key             Location/Qualifiers
FT   Region          6..40
FT                   /note= "hinge region"
FT   Region          1..5
FT                   /note= "heavy chain variable region"
FT   Region          41..54
FT                   /note= "heavy chain constant region"
XX
PN   EP584421-A.
XX
PD   02-MAR-1994.
XX
PF   21-AUG-1992;   92EP-0402326.
XX
PR   21-AUG-1992;   92EP-0402326.
XX
PA   (CAST/) CASTERMAN C.
PA   (HAME/) HAMERS R.
XX
PI   Casterman C,  Hamers R;
XX
DR   WPI; 1994-067061/09.
XX
PT   New isolated immunoglobulin molecules devoid of light polypeptide
PT   chains - consisting of heavy polypeptide chains only, obtd. from
PT   Camelid serum, for use as antibodies
XX
PS   Disclosure; Page 19; 35pp; English.
XX
CC   This 2-chain Ig molecule lacks any light chains.  The Ig has
CC   e.g. improved solubility and aggregate much less than heavy chains
CC   of 4-chain IgS.  The Igs can be used normally for e.g. diagnosis,
CC   therapy, in vaccines, for isolation and purification of antigens
CC   and in the production of anti-idiotype antibodies.
XX
SQ   Sequence   54 AA;


  Query Match             19.2%;  Score 58;  DB 15;  Length 54;
  Best Local Similarity   31.6%;  Pred. No. 57;
  Matches   12;  Conservative    3;  Mismatches   23;  Indels    0;  Gaps    0;

Qy     16 LPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
          :|||        || |:|   |      |  |:|   |
Db      9 ipqpqpkpqpqpqpqpkpqpkpepectcpkcpapellg 46


RESULT  12
ABG14378
ID   ABG14378 standard; Protein; 53 AA.
XX
AC   ABG14378;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #14369.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
```

```
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS78565.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID No 44737; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   53 AA;


  Query Match             18.9%;  Score 57;  DB 22;  Length 53;
  Best Local Similarity   34.9%;  Pred. No. 71;
  Matches   15;  Conservative    6;  Mismatches   16;  Indels    6;  Gaps    1;

Qy      11 PGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPSPPAEG 53
           || | :| | |   :      :|:|:      || | : ||||
Db      12 pggvlippppsrtgrlagrgadptts------lpdgaagpaeg 48


RESULT  13
AAY01285
ID   AAY01285 standard; Protein; 41 AA.
XX
AC   AAY01285;
XX
DT   01-JUN-1999  (first entry)
XX
DE   Peptide encoded by HRGP gene cassette.
XX
KW   Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP;
KW   repetitive proline-rich protein; RPRP; arabino-galactan protein; AGP;
KW   glycopeptide; internal repeat.
XX
OS   Synthetic.
XX
PN   WO9903978-A1.
XX
PD   28-JAN-1999.
XX
PF   21-JUL-1998;   98WO-US15083.
XX
PR   20-JUL-1998;   98US-0897556.
PR   21-JUL-1997;   97US-0897556.
XX
PA   (UYOH-) UNIV OHIO.
XX
PI   Kielszewski MJ;
XX
DR   WPI; 1999-132225/11.
DR   N-PSDB; AAX27690.
XX
PT   Novel synthetic gene designed from repetitive peptide sequences - of
PT   hydroxyproline-rich glycoprotein
XX
PS   Disclosure; Fig 1; 72pp; English.
XX
CC   The invention relates to novel synthetic genes for plant gums. A new
CC   approach is described to the production of hydroxyproline-rich
CC   glycoproteins (HRGPs), repetitive proline-rich proteins (RPRPs) and
CC   arabino-galactan proteins (AGPs). Synthetic genes comprising a nucleic
CC   acid encoding the peptide (AAY01267) can be engineered for the
CC   production of repetitive glycopeptide modules in cells. The invention
CC   provided a new approach to the problem of producing plant gums that is
CC   not dependent on environmental factors and greatly simplifies the
CC   production of a variety of naturally occurring gums as well as designer
CC   gums.
XX
SQ   Sequence   41 AA;


  Query Match             18.7%;  Score 56.5;  DB 20;  Length 41;
  Best Local Similarity   43.3%;  Pred. No. 61;
  Matches   13;  Conservative    3;  Mismatches   11;  Indels    3;  Gaps    1;

Qy      21 STRSQHTQPTPEPSTAPSTSFLLPMGPSPP 50
           |||:    |:| | : |  |   |  ||||
Db       4 straspppppppppppppp---ppppspp 30


RESULT  14
AAO06362
ID   AAO06362 standard; Protein; 56 AA.
XX
AC   AAO06362;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 20254.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US04927.
XX
PR   28-FEB-2000; 2000US-0515126.
PR   18-MAY-2000; 2000US-0577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI86293.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 20254; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
```

```
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   56 AA;


  Query Match             18.7%;  Score 56.5;  DB 22;  Length 56;
  Best Local Similarity   32.7%;  Pred. No. 84;
  Matches   18;  Conservative    3;  Mismatches   27;  Indels    7;  Gaps    3;

Qy       4 SPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLP-----MGPSPPAEG 53
           ||:    |       | |:|| |  | | |   |   |  |      |  || :|
Db       4 spsakkppqkpdkshp-ssrs-hpfpppppcxtpppefxypppkgewgarpppqg 56


RESULT  15
ABB38671
ID   ABB38671 standard; Peptide; 47 AA.
XX
AC   ABB38671;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #6177 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 31306; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   47 AA;


  Query Match             18.5%;  Score 56;  DB 22;  Length 47;
  Best Local Similarity   38.3%;  Pred. No. 79;
  Matches   18;  Conservative    2;  Mismatches   23;  Indels    4;  Gaps    2;

Qy       5 PTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPST-SFLLPMGPSPP 50
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Db       1 pctvaappaaaap---peragptspspaavaapstlssscpatpcpp 44


Search completed: August 21, 2002, 10:07:44
Job time: 257 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:01:32 ; Search time 12.86 Seconds
(without alignments)
108.263 Million cell updates/sec

Title: US-09-800-909-2_COPY_201_257
Perfect score: 302
Sequence: 1 TSTSPTRSMAPGAVHLPQPV.....STSFLLPMGPSPPAEGSTGD 57

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 166652

Minimum DB seq length: 0
Maximum DB seq length: 57

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	27.5	15	1	US-08-221-583-56	Sequence 56, Appl
2	83	27.5	15	5	PCT-US95-04018-56	Sequence 56, Appl
3	82	27.2	15	1	US-08-221-583-58	Sequence 58, Appl
4	82	27.2	15	5	PCT-US95-04018-58	Sequence 58, Appl
5	81	26.8	15	1	US-08-221-583-57	Sequence 57, Appl
6	81	26.8	15	1	US-08-221-583-62	Sequence 62, Appl
7	81	26.8	15	5	PCT-US95-04018-57	Sequence 57, Appl
8	81	26.8	15	5	PCT-US95-04018-62	Sequence 62, Appl
9	80	26.5	15	1	US-08-221-583-55	Sequence 55, Appl
10	80	26.5	15	1	US-08-221-583-59	Sequence 59, Appl
11	80	26.5	15	5	PCT-US95-04018-55	Sequence 55, Appl
12	80	26.5	15	5	PCT-US95-04018-59	Sequence 59, Appl
13	79	26.2	15	1	US-08-221-583-61	Sequence 61, Appl
14	79	26.2	15	5	PCT-US95-04018-61	Sequence 61, Appl
15	78	25.8	15	1	US-08-221-583-60	Sequence 60, Appl
16	78	25.8	15	5	PCT-US95-04018-60	Sequence 60, Appl
17	69	22.8	15	1	US-08-221-583-54	Sequence 54, Appl
18	69	22.8	15	5	PCT-US95-04018-54	Sequence 54, Appl
19	59	19.5	45	1	US-08-361-920-19	Sequence 19, Appl
20	59	19.5	45	1	US-08-479-939-19	Sequence 19, Appl
21	59	19.5	45	1	US-08-483-432-19	Sequence 19, Appl
22	58	19.2	54	1	US-08-471-780C-44	Sequence 44, Appl
23	58	19.2	54	1	US-08-467-282B-44	Sequence 44, Appl
24	58	19.2	54	2	US-08-471-282A-44	Sequence 44, Appl
25	58	19.2	54	2	US-08-466-710C-44	Sequence 44, Appl
26	58	19.2	54	3	US-08-468-739C-44	Sequence 44, Appl
27	55	18.2	15	1	US-08-221-583-53	Sequence 53, Appl
28	55	18.2	15	5	PCT-US95-04018-53	Sequence 53, Appl
29	55	18.2	46	3	US-08-856-074A-39	Sequence 39, Appl
30	55	18.2	48	6	5171685-7	Patent No. 5171685
31	55	18.2	48	6	5518916-7	Patent No. 5518916
32	53.5	17.7	37	3	US-08-814-052-37	Sequence 37, Appl
33	53.5	17.7	37	3	US-08-812-829-29	Sequence 29, Appl
34	52.5	17.4	21	5	PCT-US92-10432-1	Sequence 1, Appli
35	52.5	17.4	22	1	US-08-442-542-43	Sequence 43, Appl
36	52.5	17.4	22	3	US-08-765-469-43	Sequence 43, Appl
37	50.5	16.7	53	6	5422248-4	Patent No. 5422248
38	50	16.6	16	1	US-08-366-591-15	Sequence 15, Appl
39	49.5	16.4	33	1	US-08-237-716-11	Sequence 11, Appl
40	49.5	16.4	40	1	US-08-099-354-1	Sequence 1, Appli
41	49.5	16.4	40	2	US-08-288-059-7	Sequence 7, Appli
42	49.5	16.4	41	1	US-08-361-920-13	Sequence 13, Appl
43	49.5	16.4	41	1	US-08-479-939-13	Sequence 13, Appl
44	49.5	16.4	41	1	US-08-483-432-13	Sequence 13, Appl
45	49	16.2	16	1	US-08-471-033-47	Sequence 47, Appl

ALIGNMENTS

```
RESULT   1
US-08-221-583-56
; Sequence 56, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-56


  Query Match             27.5%;  Score 83;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 HLPQPVSTRSQHTQP 29
           |||||||||||||||
Db       1 HLPQPVSTRSQHTQP 15


RESULT   2
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PCT-US95-04018-56
; Sequence 56, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-56


  Query Match             27.5%;  Score 83;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 HLPQPVSTRSQHTQP 29
           |||||||||||||||
Db       1 HLPQPVSTRSQHTQP 15


RESULT   3
US-08-221-583-58
; Sequence 58, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-58


  Query Match             27.2%;  Score 82;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0051;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      24 SQHTQPTPEPSTAPS 38
           |||||||||||||||
Db       1 SQHTQPTPEPSTAPS 15


RESULT   4
PCT-US95-04018-58
; Sequence 58, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
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;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-58


  Query Match             27.2%;  Score 82;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0051;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      24 SQHTQPTPEPSTAPS 38
           |||||||||||||||
Db       1 SQHTQPTPEPSTAPS 15


RESULT   5
US-08-221-583-57
; Sequence 57, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-57


  Query Match             26.8%;  Score 81;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 STRSQHTQPTPEPST 35
           |||||||||||||||
Db       1 STRSQHTQPTPEPST 15


RESULT   6
US-08-221-583-62
; Sequence 62, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-62


  Query Match             26.8%;  Score 81;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      36 APSTSFLLPMGPSPP 50
           |||||||||||||||
Db       1 APSTSFLLPMGPSPP 15


RESULT   7
PCT-US95-04018-57
; Sequence 57, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-57


  Query Match             26.8%;  Score 81;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 STRSQHTQPTPEPST 35
           |||||||||||||||
Db       1 STRSQHTQPTPEPST 15


RESULT   8
PCT-US95-04018-62
; Sequence 62, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-62


  Query Match             26.8%;  Score 81;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      36 APSTSFLLPMGPSPP 50
           |||||||||||||||
Db       1 APSTSFLLPMGPSPP 15


RESULT   9
US-08-221-583-55
; Sequence 55, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-55


  Query Match             26.5%;  Score 80;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0083;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 GAVHLPQPVSTRSQH 26
           |||||||||||||||
Db       1 GAVHLPQPVSTRSQH 15
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RESULT  10
US-08-221-583-59
; Sequence 59, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-59


  Query Match             26.5%;  Score 80;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0083;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      27 TQPTPEPSTAPSTSF 41
           |||||||||||||||
Db       1 TQPTPEPSTAPSTSF 15


RESULT  11
PCT-US95-04018-55
; Sequence 55, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-55


  Query Match             26.5%;  Score 80;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0083;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      12 GAVHLPQPVSTRSQH 26
           |||||||||||||||
Db       1 GAVHLPQPVSTRSQH 15


RESULT  12
PCT-US95-04018-59
; Sequence 59, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
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;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-59


  Query Match             26.5%;  Score 80;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0083;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      27 TQPTPEPSTAPSTSF 41
           |||||||||||||||
Db       1 TQPTPEPSTAPSTSF 15


RESULT  13
US-08-221-583-61
; Sequence 61, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-61


  Query Match             26.2%;  Score 79;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 PSTAPSTSFLLPMGP 47
           |||||||||||||||
Db       1 PSTAPSTSFLLPMGP 15


RESULT  14
PCT-US95-04018-61
; Sequence 61, Application PC/TUS9504018
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    APPLICANT:  Kruszynski, Marian
;    APPLICANT:  Mervic, Miljenko
;    APPLICANT:  Weber, Robert W.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  Norris
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04018
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,580
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,583
;      FILING DATE:  01-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,581
;      FILING DATE:  01-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0232
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-04018-61


  Query Match             26.2%;  Score 79;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 PSTAPSTSFLLPMGP 47
           |||||||||||||||
Db       1 PSTAPSTSFLLPMGP 15


RESULT  15
US-08-221-583-60
; Sequence 60, Application US/08221583
; Patent No. 5486595
;  GENERAL INFORMATION:
;    APPLICANT:  Heavner, George A.
;    TITLE OF INVENTION:  Tumor Necrosis Factor Inhibitors
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
```

```
;      STREET:  One Liberty Place  46th Floor
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19403
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25:mdctcMod.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,583
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  CCOR-0185
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-221-583-60


  Query Match             25.8%;  Score 78;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      30 TPEPSTAPSTSFLLP 44
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Db       1 TPEPSTAPSTSFLLP 15


Search completed: August 21, 2002, 10:07:08
Job time: 336 sec
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